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(54) Title: NEMATODE-INDUCED GENES IN TOMATO

(57) Abstract

The present invention provides nucleic sequences from genes which are preferentially expressed in feeding site cells. These sequences can be used to produce transgenic plants resistant to nematode infection.

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NEMATODE-INDUCED GENES IN TOMATO

BACKGROUND OF THE INVENTION

This invention was made with Government support under Grant No. 89-37263-4355 awarded by the U.S. Department of Agriculture. The Government has certain rights in this invention.

The present invention relates to methods and nucleic acid compositions for the production of transgenic plants resistant to nematodes. In particular, it relates to nematode-resistant transgenic plants comprising sequences from nematode-induced genes.

Plant parasitic nematodes significantly affect the productive capability of the world's farmlands. They reduce the yield of the world's forty major food staples and cash crops by an average of 12.3%, with losses substantially higher for some commodities (*e.g.*, 20.6% for tomato). In the U.S. the reduced yields cause losses of $5.8 billion annually.

Especially significant in terms of crop losses are the sedentary endo-parasites, cyst nematodes (*Globodera* spp. and *Heterodera* spp.) and root-knot nematodes (*Meloidogyne* spp.). Cyst nematodes generally infect potatoes, soybeans, sugar beets, and wheat. Root-knot nematodes affect over 2,000 species of plants, including most of the major crops in the world.

Root-knot nematodes and cyst nematodes have similar life-cycles. Infection occurs after larvae hatch in the soil, invade the root and migrate intercellularly to the developing vascular cylinder where permanent feeding sites are established. Mature feeding sites are characterized by the presence of multinucleate cells, termed "giant cells" in root-knot nematode infections and "syncytia" in cyst nematode infections. These large, avacuolate cells with extensively remodeled cell walls are metabolically active and serve as the obligate nutritive source for the developing nematode. Giant cell

formation, coupled with limited proliferation of nearby pericycle and cortical cells results in the characteristic root-knot gall.

Today, nematode infections are controlled primarily using chemical nematicides. These compounds are generally very toxic and have been suspected of causing environmental damage. These concerns have prompted efforts to find other methods of controlling nematodes in economically important crop plants. The present invention addresses these and other needs.

SUMMARY OF THE INVENTION

The term "antisense orientation" refers to the orientation of nucleic acid sequence from a structural gene that is inserted in an expression cassette in an inverted manner with respect to its naturally occurring orientation. When the sequence is double stranded, the strand that is the template strand in the naturally occurring orientation becomes the coding strand, and vice versa.

The term "expression" refers to the transcription and translation of a structural gene so that a protein is synthesized.

A "feeding site cell" is an enlarged cell in a plant root which is induced in response to nematode infection and provides nourishment to the developing nematode. Feeding site cells arising in response to root-knot nematode infections are termed giant cells, while those arising in response to cyst nematode infections are termed syncytia.

A "nematode-induced" gene is one which is preferentially expressed in feeding site cells as compared to surrounding normal root tissue. The gene may be one which is normally expressed in other plant tissues (*e.g.*, leaf, cotyledon, apex, or hypocotyl) and is up-regulated in feeding site cells. Alternatively, the gene may be one that is not normally expressed in other plant

tissues, but is expressed only in response to nematode infection.

A "nematode-responsive" promoter is one which drives expression of an operably linked polynucleotide sequence only in, or substantially only in, feeding site cells. A promoter is considered to be nematode responsive if the level of expression of the operably linked polynucleotide sequence in cells other than feeding site cells is not sufficient to effectively disrupt cellular function. Thus, for example, if the sequence encodes a protein toxic to plant cells, plant cells other than feeding site cells are not adversely affected by the presence of a construct comprising the promoter and the structural gene.

"Nucleic acids" and "polynucleotides", as used herein, may be DNA or RNA. One of skill will recognize that the sequences from nematode-induced genes used in the methods of the invention need not be identical and may be substantially identical (as defined below) to sequences disclosed here. In particular, where a polynucleotide sequence is transcribed and translated to produce a functional polypeptide, one of skill will recognize that because of codon degeneracy a number of polynucleotide sequences will encode the same polypeptide. Similarly, because amino acid residues share properties with other residues, conservative substitutions of amino acids within a polypeptide may lead to distinct polypeptides with similar or identical function.

The term "operably linked" refers to functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates transcription of RNA corresponding to the second sequence.

"Percentage of sequence identity" for polynucleotides and polypeptides is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the

polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Optimal alignment of sequences for comparison may be conducted by computerized implementations of known algorithms (*e.g.*, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI, or BlastN and BlastX available from the National Center for Biotechnology Information), or by inspection. Sequences are typically compared using either BlastN or BlastX with default parameters.

Substantial identity of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 75% sequence identity, preferably at least 80%, more preferably at least 90% and most preferably at least 95%, Typically, two polypeptides are considered to be substantially identical if at least 40%, preferably at least 60%, more preferably at least 90%, and most preferably at least 95% are identical or conservative substitutions. Sequences are preferably compared to a reference sequence using GAP using default parameters.

Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine,

valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that polynucleotide sequences are substantially identical is if two molecules selectively hybridize to each other under stringent conditions. Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically stringent conditions for a Southern blot protocol involve washing at 65°C with 0.2XSSC.

The term "plant" includes whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds and plant cells. The class of plants which can be used in the method of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants. It includes plants of a variety of ploidy levels, including polyploid, diploid and haploid.

A "polypeptide which inhibits nematode infection" is any polypeptide which when present in a cell infected by a nematode prevents formation of a feeding cell and/or

development of the nematode. Polypeptides which have this property can act by killing or disabling the infected cell or the nematode itself. Alternatively, the polypeptide may inhibit the activity of proteins and other compounds necessary for feeding cell development. A number of polypeptides which inhibit nematode infection are described below.

The term "promoter" refers to a region of DNA upstream from the structural gene and involved in recognition and binding RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells.

The phrase "selectively hybridizing to", refers to a hybridization between a probe and a target sequence in which the probe binds substantially only to the target sequence when the target is in a heterogeneous mixture of polynucleotides and other compounds. Such hybridization is determinative of the presence of the target sequence. Although the probe may bind other unrelated sequences, at least 90%, preferably 95% or more of the hybridization complexes formed are with the target sequence.

The phrase "substantially pure" or "isolated" when referring to a polynucleotide or protein, means a chemical composition which is free of other subcellular components of the organism from which it is derived, *e.g.*, tomato plants. Typically, a compound is substantially pure when at least about 85% or more of a sample exhibits a single polypeptide backbone, or polynucleotide sequence. Minor variants or chemical modifications may typically share the same polypeptide sequence. Depending on the purification procedure, purities of 85%, and preferably over 95% pure are possible. Nucleic acid and protein purity or homogeneity may be indicated by a number of means well known in the art, such as gel electrophoresis and the like.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a flow diagram outlining the strategy used to construct the cDNA library enriched for nematode-induced sequences.

Figure 2 shows the carboxyl terminus domain (CTD) of the deduced DB#117 gene product, aligned to show the heptamer repeat. The asterisk represents the carboxy terminus. In bold below is the canonical heptamer repeat for the CTD of the largest subunit of RNA polymerase II.

Figure 3 shows the deduced DB#280 gene sequence (bold) aligned with Myb sequences from Petunia, moss, the snapdragon 315 and 308 genes, barley, *Arabidopsis*, maize, *Drosophila*, and human. Database accession numbers are in brackets. Identical amino acids are indicated, + represents conservative substitutions. None of the sequences have gaps.

Figure 4 shows alignment of the DB#226 sequence with the 3'UTR of the tobacco (*Nicotiana plumbaginiflora*) *pma*-4 gene, which encodes a plasmalemma proton ATPase.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The invention provides nucleic acid sequences from genes which are preferentially expressed in feeding site cells. These sequences can be used to produce transgenic plants resistant to nematode infection.

Although feeding site cells, such as giant cells, share features with other plant cells, notably transfer cells, they are a novel cell type, and presumably arise by a pattern of gene expression different from that in other plant cells. It has previously been speculated that gene expression in giant cells might include genes normally expressed at different developmental times or in different cell types (Bird, Mechanisms of the Meloidogyne-host interaction. In: *Nematology: from molecule to ecosystem*. (1992) F. J. Gommers, and P. W. Th. Maas, eds. ESN Inc., Dundee, Scotland).

In a survey of randomly chosen, cloned root mRNAs, Evans *et al.* (*Mol. Gen. Genet.* 214:153-157 (1988)) were unable to identify any as being root-specific. Using a differential screen, Conkling *et al.* (*Plant Physiol.* 93:1203-1211 (1990)) isolated genes encoding four, moderately to abundantly expressed, root-specific transcripts from tobacco. The expression of one of these, TobRB7, has been reported to be up-regulated in giant cells induced in tobacco by *Meloidogyne incognita* (Opperman *et al.* 1994. *Science* 263:221-223). Also using a differential screening approach, Gurr *et al.* (*Mol. Gen. Genet.* 226:361-366 (1991)) identified a gene in potato whose expression is "correlated with events in the immediate vicinity of the pathogen" (potato cyst nematode, *Globodera rostochiensis*), but the nature of this gene was not revealed.

The present invention is based in part on the isolation of genes whose expression is up-regulated in giant cells as compared to normal root tissue. Although the methods described below relate to the analysis of nematode infected cells, the same approach can be used to identify genes induced by a variety of pathogens (*e.g.*, bacteria, viruses, and fungi) in any crop plant of interest. One of skill will thus recognize that the recombinant DNA techniques for the control of nematodes described below, can also be applied to other pathogens in other crop plants.

Generally, the nomenclature and the laboratory procedures in recombinant DNA technology described below are those well known and commonly employed in the art. Standard techniques are used for cloning, DNA and RNA isolation, amplification and purification. Generally enzymatic reactions involving DNA ligase, DNA polymerase, restriction endonucleases and the like are performed according to the manufacturer's specifications. These techniques and various other techniques are generally performed according to Sambrook et al., *Molecular Cloning*

- *A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989).

I. Isolation of nematode-induced genes and nematode-responsive promoters

The isolation of nematode-induced genes from plants may be accomplished by a number of techniques. Such genes are generally isolated using techniques designed to identify sequences specific to a particular tissue or cell types (*see, e.g.*, Sambrook *et al.*) Such techniques include differential hybridization techniques as described for instance in Gurr *et al. Mol. Gen. Genet.* 226:361-366 (1991). Briefly, in differential hybridization techniques a cDNA library prepared from feeding site cells is screened with probes generated from cDNA derived from feeding site cells and normal root tissue. Those clones in the cDNA library which show increased hybridization to cDNA from feeding site cells are candidates for genes which are up-regulated in these cells. The clones identified in this way are then used to screen a genomic library to isolate the corresponding gene.

In addition, subtractive hybridization techniques can be used to prepare specific probes for screening cDNA or genomic libraries. These techniques can also be used to prepare subtracted libraries enriched for the desired sequences. Subtractive screening or cDNA cloning approaches have proven effective in identifying transcripts with differential expression profiles. To ensure that cDNAs representing transcripts expressed in low abundance are represented requires that enough cDNA remain after subtraction for efficient cloning. Methods have been developed using PCR and other techniques to ensure that low abundance transcripts are identified. A preferred subtractive hybridization technique using these modifications is described in the Example section, below.

Other techniques for the identification of nematode-induced genes can also be used. For instance,

oligonucleotide probes based on the sequences of previously identified nematode-induced genes can be used to isolate the desired gene in a cDNA or genomic DNA library. These techniques can be used to isolate homologous genes in the same or different plant species. The use of such hybridization techniques for identifying homologous genes is well known in the art and need not be described further.

Alternatively, interposon tagging can be used (Topping *et al.* 1991 *Developm.* 112:1009-1019 and Kertbundit *et al.* 1991 *Proc. Natl. Acad. Sci. USA* 88:5212-5216). In this method, a number of transgenic plants are produced each carrying a randomly integrated recombinant construct containing a promoterless reporter gene, such as β-glucuronidase (GUS). Various tissues in the plant are then analyzed for expression of the reporter gene. If the reporter gene integrates in a site downstream from a promoter primarily active in a particular tissue, cells in the tissue will contain the reporter gene product. Promoter sequences and genes that are primarily active in feeding site cells can thus be identified.

Once a desired genomic clone is identified, the 5' sequences can be analyzed to identify the promoter sequence from the gene. This can be accomplished using deletion analysis and a promoterless reporter gene (*e.g.*, GUS) to identify those regions which can drive expression of a structural gene.

Sequences characteristic of promoter sequences can also be used to identify the promoter. Sequences controlling eukaryotic gene expression have been extensively studied. For instance, promoter sequence elements include the TATA box consensus sequence (TATAAT), which is usually 20 to 30 base pairs upstream of the transcription start site. In most instances the TATA box is required for accurate transcription initiation. In plants, further upstream from the TATA

box, at positions -80 to -100, there is typically a promoter element with a series of adenines surrounding the trinucleotide G (or T) N G. J. Messing et al., in *Genetic Engineering in Plants*, pp. 221-227 (Kosage, Meredith and Hollaender, eds. 1983).

In addition, sequence comparison with promoters from other genes that are up-regulated in response to nematode infection can be used to identify regions of sequence homology among the genes. For example, comparison of the 5′ flanking sequences of the sequences disclosed here can be used to identify common sequences. Alternatively, other genes previously identified as being nematode-induced (*e.g.*, TobRB7) can be used.

Various methods relying on polymerase chain reaction (PCR) techniques to amplify the desired sequence can also be used. The amplified sequence is then subcloned into a vector where it is then sequenced using standard techniques. For example, PCR can be used to amplify a DNA sequence using a random 5′ primer and a defined 3′ primer. The 3′ primer is based on the sequence of a cDNA isolated by differential screening or subtractive hybridization. The random 5′ primer is then used to amplify genomic DNA upstream of the cDNA, to identify promoter sequences. Alternatively, genomic DNA can be cut at a suitable restriction site (determined from Southern blotting experiments) upstream from presumed promoter elements. A linker sequence is attached to the fragments and used as a specific 5′ PCR priming site, along with the 3′ primer based on the cDNA sequence.

Another approach is to use inverse PCR in which genomic DNA is restricted to generate a sticky ended molecule that spans known sequences at the 5′ end of the gene and unknown promoter sequences. The DNA is ligated into circles and PCR amplified with a specific divergent primer pair designed from the cDNA sequence.

II. Production of nematode-resistant plants

Nematode-induced sequences, such as those described here, can be used in a variety of methods using recombinant DNA techniques for the control of nematodes in plants. For instance, the promoters from genes identified here can be used to drive expression of desired sequences in feeding site cells. The sequences can be structural genes encoding desired polypeptides or can be sequences which transcribe RNAs capable of inhibiting the expression of genes required for feeding site cell development. The promoters are used to ensure that the desired sequences are expressed only or substantially only in feeding site cells.

The polypeptides encoded by the structural genes will preferably prevent the development of the nematode in the plant in some way. For instance, the polypeptide may interfere with the transduction of the signal that leads to feeding cell formation in the host. Alternatively, polypeptides which have nematicidal or herbicidal activity can be used. The inhibitory RNAs may function in antisense suppression, sense suppression or as ribzoymes.

A. Construction of expression vectors

The methods required for the recombinant expression of desired genes in transgenic plants are well known to those of skill in the art. Briefly, expression cassettes comprising a promoter from a nematode-induced gene operably linked to desired sequence such as a structural gene encoding a desired protein is introduced into the plant. Construction of appropriate expression vectors is carried out using standard techniques.

The minimal requirements of the vector are that the desired nucleic acid sequence be introduced in a relatively intact state. Thus, any vector which will produce a plant carrying the introduced DNA sequence should be sufficient. The selection of vectors and methods to construct them are commonly known to persons

of ordinary skill in the art and are described in general technical references (See, in general, *Methods in Enzymology* Vol. 153 ("Recombinant DNA Part D") 1987, Wu and Grossman Eds., Academic Press.

The recombinant vectors of the present invention typically comprise an expression cassette designed for initiating transcription of the desired polynucleotide sequences in plants. Companion sequences, of bacterial origin, are also included to allow the vector to be cloned in a bacterial host. The vector will preferably contain a broad host range prokaryote origin of replication. A selectable marker should also be included to allow selection of bacterial cells bearing the desired construct. Suitable prokaryotic selectable markers include resistance to antibiotics such as kanamycin or tetracycline.

Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art. For instance, in the case of *Agrobacterium* transformations, T-DNA sequences will also be included for subsequent transfer to plant chromosomes.

For expression of polypeptides in plants, the recombinant expression cassette will contain, in addition to the desired polynucleotide sequence and the promoter derived from a nematode-induced gene, a transcription initiation site (if the sequence to be transcribed lacks one), and a transcription termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette are typically included to allow for easy insertion into a pre-existing vector.

The promoters can be modified as necessary to ensure that the desired polynucleotide sequence is expressed substantially only in response to nematode infection. A number of methods can be used to identify those sequences within a given promoter that are responsible for a specific response to nematode infection. As noted above, sequences shared by promoters of nematode-induced genes

can be used to design promoters with the desired specificity. Alternatively, a reporter gene (*e.g.*, GUS) can be operably linked to various deletion mutants of the promoter sequence and the ability of the modified promoters to direct expression in feeding site cells and other tissues can be assayed (*see, e.g.*, WO 93/06710).

In the construction of heterologous promoter/structural gene combinations, the promoter is preferably positioned about the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

As noted above, an expression cassette should also contain a transcription termination region downstream of the structural gene to provide for efficient termination. The termination region may be obtained from the same gene as the promoter sequence or may be obtained from different genes.

If the mRNA encoded by the structural gene is to be efficiently translated, polyadenylation sequences are also commonly added to the vector construct. Alber and Kawasaki, *Mol. and Appl. Genet*, 1:419-434, 1982. Polyadenylation sequences include, but are not limited to the *Agrobacterium* octopine synthase signal (Gielen et al., *EMBO J.*, 3:835-846, 1984) or the nopaline synthase signal (Depicker et al., *Mol. and Appl. Genet*, 1:561-573, 1982).

The vector will also typically contain a selectable marker gene by which transformed plant cells can be identified in culture. Usually, the marker gene will encode antibiotic resistance. These markers include resistance to G418, hygromycin, bleomycin, kanamycin, and gentamicin. After transforming the plant cells, those cells having the vector will be identified by their

ability to grow in a medium containing the particular antibiotic.

Polypeptides which inhibit nematode infection

As noted above, the promoter can be used to drive expression of structural genes encoding polypeptides which inhibit nematode infection. A variety of structural genes encoding protein or polypeptide products which inhibit the infection by, for instance, inhibiting the process of feeding cell development, promoting a plant defense response, killing or disabling the plant cell, or killing the nematode itself can be used. It is preferred, particularly where the plant is a food plant, that the polypeptide be non-toxic to animals, and particularly be non-toxic to humans.

Polypeptides which inhibit feeding cell formation will typically be competitive inhibitors of the nematode signals which induce feeding cell formation. For instance, proteins encoded by the sequences disclosed here, which are shown to be involved in signal transduction, can used to design highly specific inhibitors of feeding cell formation. In this embodiment of the invention, the polypeptides preferably have sequences substantially identical to those portions of the signal transducing proteins which interact with the appropriate ligand molecule. The signal transducing proteins can also be used to design non-protein inhibitors, which can be used as traditional nematicidal agents.

Genes which produce antibodies immunoreactive with molecules in the plant cell (*e.g.*, proteins, carbohydrates, and nucleic acids) can also be used to inhibit the development of feeding cells (*see, e.g.*, Huse *et al.*, *Science* 246, 1275-1281 (1989)). As used here the term "antibody" refers to a variety of forms of immunoglobulin molecules besides whole antibodies, including for example, Fv, Fab, and $F(ab)_2$ fragments, single chains and the like. Plant proteins to which such

antibodies can be directed include, but are not limited to, RNA polymerase, respiratory enzymes, cytochrome oxidase, Krebs cycle enzymes, protein kinases, aminocyclopropane-1-carboxylic acid synthase, and enzymes involved in the shikimic acid pathway such as enolpyruvyl shikimic acid-5-phosphate synthase. Nematode proteins or nematode-induced molecules can also be targeted. Examples include low molecular weight compounds, with few or no features in common with normal plant products, such as hormones or elements of the signal transduction pathway. Products that play a role in signaling between plants and other organisms (*e.g.*, the nod factor) can also be targeted. Preferred antigens include compounds secreted through the nematode's feeding stylet that initiate and/or maintain feeding cells.

Another class of structural genes which can be used in the invention are those induced by plant pathogens (*e.g.*, nematodes, bacteria, fungi and the like) and that elicit a hypersensitive or other defense responses in plants. Thus, a gene which is normally responsive to a particular pathogen (or to nematodes in another plant species) is made responsive to nematode infection in the transgenic plant. An example of a suitable nematode-inducible gene is the Mi gene from tomato. Examples of suitable genes responsive to other pathogens are reviewed in Stintz *et al. Biochemie* 75:687-706 (1993).

Phytotoxic polypeptides used in the invention may either kill the plant cell in which they are expressed or simply disable the cell so that it is less capable of supporting the pathogen. Examples of suitable structural genes encoding phytotoxic polypeptides include genes encoding enzymes capable of degrading nucleic acids (*e.g.*, nucleases, restriction endonucleases micrococcal nuclease, and ribonucleases such as Rnase A and barnase) and enzymes which attack proteins (*e.g.*, trypsin, pronase A, carboxypeptidase, endoproteinase Asp-N, endoproteinase Glu-C, and endoproteinase Lys-C). Other examples include

toxins from plant pathogens (*e.g.*, phaseolotoxin, tabtoxin, and syringotoxin), lipases from porcine pancrease and *Candida cyclindracea*, as well as membrane channel proteins such as glp F and connexins.

Structural genes which are specifically target nematodes include those encoding *Bacillus thuringiensis* toxins as described, for instance, in EP 517, 367 A1. Other proteins include proteinase inhibitors such as cowpea trypsin inhibitor as described in WO 92/15690 or proteins which affect nematode sensory behavior such as miraculin.

Sequences which inhibit expression of nematode-induced genes

Recombinant techniques can also be used to inhibit expression of particular genes which are required for development of feeding site cells. In these techniques inhibitory RNAs (*i.e.*, those which inhibit the expression of target genes) are transcribed in feeding site cells. Promoters from nematode-induced genes are preferably used to direct transcription of the inhibitory RNA sequences only in feeding site cells and thus prevent development of the pathogen. If the target gene is expressed only in feeding site cells, other constitutive or inducible promoters well known to those of skill in the art can also be used. For instance, the 35S promoter from cauliflower mosaic virus may be used. Alternatively, inducible promoters which direct expression only in root tissue can be used.

In some embodiments, antisense regulation of the gene can be used. To accomplish this, a polynucleotide sequence from the desired gene is cloned and operably linked to a promoter (*e.g.*, a promoter from a nematode-induced gene) such that the anti-sense strand of RNA will be transcribed. The construct is then transformed into plants and the anti-sense strand of RNA is produced. In plant cells, it has been shown that anti-sense RNA inhibits gene expression by preventing the accumulation

of mRNA which encodes the enzyme of interest, see, e.g., Sheehy et al., *Proc. Nat. Acad. Sci. USA*, 85:8805-8809 (1988), and Hiatt et al., U.S. Patent No. 4,801,340.

In other embodiments, cloned polynucleotide sequences configured such that the sense-strand of RNA is produced can be used to block the transcription of target genes in plants. For an example of the use of this method to modulate expression of endogenous genes see, Napoli et al., *The Plant Cell* 2:279-289 (1990), and U.S. Patent No. 5,034,323.

A third approach is the use of catalytic RNA molecules or ribozymes. Ribozymes can be designed to specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified in the literature. One class of ribozymes is derived from a number of small circular RNAs which are capable of self-cleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and subterranean clover mottle virus. Analysis of the self-cleaving RNAs reveals the presence of a conserved regions necessary for cleavage and allows the design of ribozymes specific for a target RNA. The design and use of target RNA-specific ribozymes is described in Haseloff et al. *Nature*, 334:585-591 (1988).

The inhibitory nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the target nematode-induced gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors for use in the present invention can be designed such that the inhibitory effect applies to one or more genes within a family of genes exhibiting homology or substantial homology to the target gene. Similarly, segments from nematode-induced genes from tomato can be used to inhibit expression of homologous genes in different plant species, e.g., using sense or antisense suppression techniques described herein either directly or as a means to obtain the corresponding sequences to be used to suppress the gene.

The introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA. Generally, higher homology can be used to compensate for the use of a shorter sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments will be equally effective. Normally, a sequence of between about 30 or 40 nucleotides and about 2000 nucleotides should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of at least about 500 nucleotides is especially preferred.

B. Plant Transformation

The various DNA constructs described above may be introduced into the genome of the desired plant by a variety of conventional techniques. For example, the DNA construct may be introduced directly into the genomic DNA of the plant cell using polyethylene glycol precipitation (Paszkowski et al. *Embo J.* 3:2717-2722 (1984)) electroporation and microinjection of plant cell protoplasts (Fromm et al. *Proc. Natl. Acad. Sci. USA*

82:5824 (1985)), or the DNA constructs can be introduced into plant tissue using ballistic methods, such as DNA particle bombardment (Klein et al. *Nature* 327:70-73 (1987)). Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. For a review of gene transfer methods for plant and cell cultures *see*, Potrykus *CIBA Found. Symp.* 154:198 (1990).

Agrobacterium tumefaciens-meditated transformation techniques are the most commonly used techniques for transferring genes into plants. These techniques are well described in the scientific literature. See, for example Horsch et al. *Science* 233:496-498 (1984), Fraley et al. *Proc. Natl. Acad. Sci. USA* 80:4803 (1983), and Hooykaas *Plant Mol. Biol.* 13:327-336 (1989).

All species which are a natural plant host for *Agrobacterium* are transformable *in vitro*. Most dicotyledonous species can be transformed by *Agrobacterium*. Monocotyledonous plants, and in particular, cereals, are not natural hosts to *Agrobacterium*. There is growing evidence now that certain monocots can be transformed by *Agrobacterium*. Using novel experimental approaches cereal species such as rye (de la Pena et al., *Nature* 325:274-276, 1987), corn (Rhodes et al., *Science* 240:204-207, 1988), and rice (Shimamoto et al., *Nature* 338:274-276, 1989) may now be transformed.

After transformation, transformed plant cells or plants comprising the introduced DNA must be identified. A selectable marker, such as those discussed above is typically used. Transformed plant cells can be selected by growing the cells on growth medium containing the

appropriate antibiotic. The presence of opines can also be used if the plants are transformed with *Agrobacterium*.

After selecting the transformed cells, one can confirm expression of the desired transgenic structural gene or inhibitory RNA. Simple detection of mRNA encoded by the inserted DNA can be achieved by well known methods in the art, such as Northern blot hybridization. The inserted sequence can be identified using the polymerase chain reaction (PCR) and Southern blot hybridization, as well. See, e.g., Sambrook, *supra*.

Transformed plant cells (*e.g.*, protoplasts) which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired nematode resistant phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, pp. 124-176, MacMillilan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. *Ann. Rev. of Plant Phys.* 38:467-486 (1987).

One of skill will recognize that after the expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

The invention has use in producing nematode resistant cultivars of any plant susceptible to infection by these pathogens. The invention thus has use over a broad range of plants, including species from the genera *Trifolium, Medicago, Phaseolus, Pisum, Vigna, Glycine,*

Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Capsicum, Datura, Hyoscyamus, Lycopersicon, Nicotiana, Solanum, Petunia, Digitalis, Cichorium, Helianthus, Chrysanthemum, Vitus, Lactuca, Asparagus, Cucumis, Cucurbita, Malus, Pyrus, Prunus, Rosa, Fragaria, Tarro, Ananas, Musa, Cacoa, Beta, Coffea, Gossypium, THea, Dioscorea, Arachis, Citrullus, Juglans, Olea, Cannabis, Triticum, Hordeum, Avena, Festuca, Sorghum, Oryza, Secale, and Zea.

The following examples illustrate, but do not limit, the invention.

Example 1

This example describes the construction of a cDNA bank representing genes either uniquely expressed in giant cells (compared to uninfected root cells) or with elevated expression levels. The methods used here combine PCR amplification of cDNA with the efficient and sensitive phagemid subtraction methods to produce a subtracted cDNA bank from a small number of individual tomato giant cells (*see*, Bird and van der Knaap *Phytopathology* 84:299-303 (1994)). A flow chart outlining the strategy used to construct the library is shown in Figure 1.

MATERIALS AND METHODS

Culture maintenance. Giant cells and normal root tissue were isolated from *in vitro* cultured tomato *(Lycoperisicon esculentum* cv 'Rutgers Large Red') plants. Seeds were surface sterilized by vacuum infusion of 0.5% sodium hypochlorite and germinated in parafilm-sealed, petri plates on 2% GelRite containing vitamin supplemented Gamborg's B5 medium. Cultures were maintained in the dark at 26 °C. When tertiary root branches were evident (approximately 2 weeks), each dish was inoculated with 200 root-knot nematode *(Meloidogyne incognita)* eggs, surface sterilized by incubation for 10 min in 0.1% streptomycin, 0.0 1% $HgCl_2$. Nematode stocks were maintained on greenhouse grown tomato (cv 'Tropic')

plants, and eggs isolated by hypochlorite extraction (McClure *et al. J. Nematol.* 5:230 (1973)).

Root galls containing young adult female nematodes were excised from the etiolated plant-nematode cultures at 1 to 2 months post infection. Gall tissue surrounding the giant cell was dissected away and the exposed, intact nematode removed. Giant cells were resected and snap frozen at -72 °C.

RNA isolation. RNA was isolated by a modification of the method of Chomczynski and Sacchi *Anal. Biochem.* 162:156-159 (1987). Approximately 50 mg of giant cells were ground under liquid nitrogen in a micro-homogenizer (Biomedix, Middlesex, UK) and resuspended in 200 μl E-buffer (4M guanidinium isothiocyanate, 25mM sodium phosphate buffer, pH 7.4, 1% sarkosyl, 1 mM β-mercaptoethanol) at 40° C. The suspension was incubated at 40° C, 20 min, with occasional vortexing. Sodium acetate pH 4 was added to 50 mM followed by an equal volume of water saturated phenol, and the sample placed on ice for 10 min. One-tenth volume of chloroform was added and the aqueous phase recovered following centrifugation at 12,000g for 10 min at 4° C. The organic phase was back-extracted with 100 μl E-buffer containing 50 mM Na-acetate pH 4 and the aqueous phases pooled. RNA was recovered by ethanol precipitation, dried *in vacuo* and dissolved in water.

Normal root RNA was extracted from uninfected tissue cultured seedlings grown in parallel and harvested at the same times as giant cells. Freshly harvested tissue was frozen in liquid nitrogen and ground in a mortar and pestle. E-buffer was added at two ml per gram fresh weight of tissue.

cDNA synthesis. Poly-A (+) RNA was captured from giant cell total RNA on oligo-dT_{25} coupled paramagnetic beads (Dynal Inc., Great Neck, N.Y.) according to the manufacturers instructions. Bead-bound RNA was washed twice with 2.5 times the original bead suspension volume

of first strand cDNA synthesis buffer (50 mM Tris HCl pH 8.0, 50 mM KCl, 10 mM $MgCl_2$) and cDNA was synthesized on the bead to produce a solid phase primary cDNA pool. First and second strand synthesis and end repair reactions were performed using the Riboclone cDNA synthesis system (Promega, Madison, WI) according to manufacturers suggestions. Beads were kept in suspension during the synthesis reactions by shaking at 350 rpm.

Oligonucleotides P35 (GTAAGCGGCCGCAGCGTCAGTAACTC, Seq. I.D. No.:110) and P36 (TACTGACGCTGCGGCCGCTTAC, Seq. I.D. No.:111) were annealed using standard conditions (Wu *et al. Meth. Enzymol.* 152:343-349 (1987)). This formed a double stranded adapter molecule, blunt at one end and with a non-complementary, four-base overhang at the opposite end, with an internal *Not*I site. P36 was end-labeled prior to annealing using polynucleotide kinase. Annealed adapter was ligated onto the free end of the bead-bound dscDNA at 15° C for 16 h with shaking at 350 rpm. Unligated adapter was removed from the cDNA by washing with sterile water until free counts were no longer detected in the wash.

Second strand cDNA was eluted from bead-bound first strand by heating to 94° C for three minutes. The beads were then snap chilled on ice and the aqueous phase removed from the beads. cDNA yield was estimated by liquid scintillation counting of an aliquot of the eluate. An additional batch of second strand cDNA was synthesized on the beads by primer extension with P36. Following elution, this material was pooled with the previously synthesized second strand cDNA. Pooled cDNA was converted to double stranded form by extension from the poly-A tract at the 3'-end with P39 primer [ACTCTTGGGCCGAGTTGGCC$(T)_{15}$] (Seq. I.D. No.:112). The dscDNA was purified from excess P39 by spin column chromatography over Sephadex G-50 equilibrated with 200 mM NaCl.

PCR amplification. One fourth of the cDNA was amplified by 15 cycles of PCR (94° C, 2 min; 58° C, 1 min; 72° C, 5 min) using primers P40 [ACTCTTGGGCCGAGTTGGCC$(T)_4$] (Seq. I.D. No.:113) and P36. Amplification products were fractionated on 1% LMP agarose and size ranges of DNA (400 - 700 bp, 700 bp - 1.3 kb, 1.3 kb - 5 kb) resected and eluted by Gelase digestion (Epicentre Technologies, Madison, WI). One-fifth of each size class was re-amplified by 10 cycles of PCR, using the same conditions as the original amplification. Each reaction was diluted five fold onto fresh reaction mix, and amplified a further 5 cycles. The 400 - 700 bp, 700 bp 1.3 kb fractions faithfully re-amplified, and were pooled.

cDNA cloning. Single stranded amplification products were removed by mung bean nuclease digestion, and the cDNA was cut with *Not*I and *Sfi*I. Fifty ng of restricted cDNA insert was ligated into 300 ng of dephosphorylated, *Not*I-*Sfi*I digested pGem 11zf(+) vector (Promega, Madison, WI). The ligation reaction was phenol extracted, ethanol precipitated, resuspended in 4 µl water, and electroporated at 200Ω, 25 µF, 18.8 kV/cm into 200 µl of electrocompetent *E. coli* DH12s cells (BRL, Gaithersburg, MD). Cells were incubated for 40 minutes in 100 ml SOC medium at 37° C with shaking (350 rpm) and an aliquot was removed to determine the number of primary transformants. Ampicillin was added to 50 µg per ml and the culture grown to an A_{600} of 0.1. Two milliliters were removed, grown overnight at 37° C and stored as a glycerol stock. M13K07 phage were added to the main culture at an moi of 10, and the culture grown for a further 2 h. Phage infected cells were selected by addition of kanamycin to 70 µg/ml, and the culture incubated with vigorous shaking at 37° C for 15 h.

Recombinant M13 virions were harvested by polyethylene glycol precipitation, and ssDNA prepared and resuspended in 200 µl water. The sample was digested

with *Hin*dIII and ssDNA purified by fractionation on LMP agarose.

Driver preparation. A solid phase cDNA pool was prepared from 75 μg of uninfected-root total RNA and 10 ng of the resultant double stranded cDNA subjected to 15 cycles of PCR, exactly as described for the giant cell library, except the dTTP concentration was reduced to 75 μM and biotin-16-dUTP (Boehringer Mannheim, Indianapolis, IN) added to 25 μM (Lebeau *et al. Nuc. Acids Res.* 19:4778 (1991)). The reaction was diluted five fold and PCR amplification continued for 5 cycles. The final yield of biotinylated cDNA was ~5 μg.

Subtraction and transformation. Biotinylated root cDNA (4 μg) was coprecipitated with 2 μg M13 DNA with giant cell cDNA inserts, giving a ten fold molar excess of driver to insert. The DNA was resuspended in 20 μl water, and 0.5 μg oligo-dT_{15} added. One microliter of 2 X hybridization solution (400mM NaCl, 100 mM Tris HCl pH 7.5, 4 mM EDTA) was added, and the mixture dried *in vacuuo* to 2 μl. The solution was covered with a drop of mineral oil, heated to 94° C 5 min, and incubated 65° C for 25 h.

The annealing reaction was diluted to 50 μl with 0.5 X SSC and then incubated at room temp for 30 min with 600 μl streptavidin coated paramagnetic beads (Promega, Madison WI), previously equilibrated to 0.5 X SSC. Beads were separated from the solution on a magnetic stand, and the binding step repeated. Oligo dT_{15} was removed from unbound ssDNA by fractionation on Sephadex G-50/200 mM and salts removed by fractionation on water equilibrated Sephadex G-50. ssDNA was transformed to double stranded form by Klenow extension from P46 primer [GGCCAAGTTGGCC$(T)_5$] (Seq. I.D. No.:114), de-salted on water saturated Sephadex G-50, dried to 3 μl *in vacuuo* and electroporated into *E. coli* DH12s cells. Cells were recovered for one hour in SOC medium and plated with an X-gal/IPTG screen. Insert containing colonies were

picked into individual wells of 96 place microtiter plates and glycerol stocks prepared.

Library analysis. Glycerol stocks were replica-stamped onto nitrocellulose membranes and were probed with nick-translated genomic tomato and nematode DNA and cDNA inserts using standard conditions (Wahl *et al. Proc. Natl. Acad. Sci. USA* 76:3683-3687'(1979)).

ssDNA was prepared from recombinants by rescue with the helper phage M13K07 and subjected to sequencing using the dideoxy chain-termination method (Sanger *et al., Proc. Natl. Acad. Sci. USA* 74:5463 (1977)). Hybridization probes for Southern and RNA dot blot analyses were prepared by primer extension of single stranded templates with universal sequencing primer. Tomato and nematode genomic DNA was prepared by grinding in liquid nitrogen followed by proteinase K digestion and phenol/chloroform extraction.

RESULTS

cDNA synthesis. Fifty one milligrams of essentially pure giant cells were accumulated by dissection. Based on comparative ethidium bromide fluorescence, the yield of total RNA from this sample was estimated to be 11 μg. This represents a yield per gram fresh weight of tissue of approximately 4 fold higher than we obtain from cultured whole roots, and possibly is a reflection of increased transcriptional activity in giant cells.

Performing the cDNA synthesis on paramagnetic beads provided a number of advantages over liquid synthesis, including the ability to readily recover poly-A(+) RNA and cDNA into essentially zero volume. Because the bead effectively blocked one end, addition of a *Not*I adapter after cDNA synthesis was restricted to the 5'-end (with respect to the message). Additionally, the use of solid phase cDNA synthesis provided a reusable pool of first strand cDNA.

Based on incorporation of ^{32}P-labeled P36 (half of the adapter), conversion of poly-A(+) RNA into eluted

second strand cDNA was 24%. Subsequent re-synthesis of second strand cDNA corresponded to a 15% conversion of poly-A(+) RNA. It is likely that this reduced efficiency resulted from inefficient priming. Conversion of pooled, eluted second strand cDNA to double stranded form by priming with an oligo-dT-anchored, *Sfi*I primer (P39) yielded 43 ng of double stranded cDNA. Analysis of an aliquot by electrophoresis on alkaline agarose revealed an average size of 800 bases for this cDNA pool, with a portion extending larger.

Pilot experiments indicated that, under our conditions, the rate of amplification began to diminish between 10 and 15 rounds of PCR while, in pari passu, the amount of single stranded product increased. Consequently, the giant cell cDNA was subjected to only 15 cycles of PCR amplification prior to size fractionation. The size classes were re-amplified and single stranded strand amplification products removed by mung bean nuclease digestion prior to cloning. Comparison of cDNA before and after nuclease treatment indicated that up to two thirds of the amplified cDNA, primarily the larger material, consisted of single strand product. The average size of the final cDNA population was about 300 bp, with a range of 200 to 500 bp. Preferential extension of smaller cDNAs over larger ones as PCR progresses has been observed previously (Belyavsky *et al. Nuc. Acids Res.* 17:2919-2932 (1989)).

Cloning. To maximize the efficiency of the cloning step, and also to eliminated the possibility of cloning uninfected-root driver cDNA, amplified giant cell cDNA was ligated into a phagemid vector. A test plating of the library at this stage indicated that it contained 1.4 X 10^6 transformants. Following conversion to single stranded form by rescue with M13K07, the cloned giant cell cDNAs were annealed with normal-root cDNA driver to a Cot value of 500. Using a k value for a typical mammalian cell (15,000 unique transcripts), the fraction

of cDNAs common both to uninfected roots and giant cells that have annealed at Cot 500 is 96.5%.

After the annealed cDNA had been removed, the single stranded recombinants were converted to double stranded form. Transformation by electroporation of double stranded plasmid DNA has been shown to be several hundred fold more efficient than single stranded plasmid DNA. We utilized a primer which spans the *SfiI* cloning site and the poly-A tail of the insert. This primer is not complementary to either insert-minus or to incorrectly oriented insert-containing clones. Production of double stranded plasmid DNA prior to transformation with this primer allowed for more efficient cloning of genuine subtracted clones over insert-minus or aberrant clones which may have escaped the subtraction procedure.

Following transformation, 287 insert-containing clones, as determined by blue/white colony screening, were recovered. This corresponded to an overall enrichment of 4,860 fold of giant cell sequences over normal root sequences present in the cDNA library. This figure is substantially higher than is typically obtained by subtraction.

Library analysis. A variety of criteria were used to assess the overall quality of the subtracted library. Insert size was determined by restriction analysis. Inserts resected from ten randomly selected clones ranged in size from 200 to 500 bp in length. Seven of these probes were also hybridized back to the entire library. One clone detected two recombinants; the remaining six probes detected only the clones from which they were constructed. This result suggests that the complexity of the subtracted library might be high.

The total number of highly repeated genomic sequences represented in the library was determined by hybridization of replica filters with nick translated tomato total genomic DNA. Forty two of the 287 clones gave a high signal. Four of these clones were sequenced;

three were derived from 25S rRNA and one from 16S rRNA. To further confirm that clones not detected in this assay were indeed derived from low copy number genes, genomic Southerns were performed using 36 randomly selected clones as probes. Hybridization banding patterns identified one apparently multicopy gene. However, most appear to be low copy or unique genes. These results also confirm that the clones are of plant origin. To determine the number of contaminating nematode sequences in the library, the replica filters were probed with nick-translated *Meloidogyne incognita* total genomic DNA. One colony gave a signal detectable above background. A second clone encoding a nematode transcript was subsequently identified by genomic blotting.

Dot blots of RNA samples isolated from tomato tissues (galls and whole mature roots from tissue culture, mature leaf from green-house grown plants, and cotyledons, hypocotyls and roots from one-week-old seedlings) were hybridized with probes synthesized from randomly selected giant cell cDNA clones. In these experiments, 5 μg of total RNA isolated from various tomato tissues was blotted onto nitrocellulose and hybridized with primer extended ^{32}P labeled antisense probes. Hybridization probes were prepared by primer extension of half of the annealed sequencing DNA template in the presence of α-[^{32}P]-dCTP. The specific activity of these probes typically was 2 X 10^9 dpm/μg. Filters were probed using standard conditions (Wahl *et al. Proc. Natl. Acad. Sci. USA* 76:3683-3687 (1979)). The presence of equal amounts of target RNA in each dot was confirmed by probing with ribosomal sequences. The exposure times varied significantly between the different filters. This variation is indicative of differences in transcript abundance because the specific activities and amount of probe used in each experiment was essentially the same.

Results from these experiments are summarized in Table 1 (clones which were not sequenced and which gave

no blot results have been omitted). Sixteen probes failed to produce a detectable hybridization signal to any of the RNA samples, suggesting that these cDNAs represent low abundance messages. The remaining cDNA clones hybridized to various subsets of the RNA samples.

Table 1. DNA sequence and RNA dot blot analysis of giant cell cDNA clones

DB#	SEQ. ID. No.	Identity[2]	Tissue source of RNA[1]					
			G	D	L	H	A	R
101	SEQ. ID. No. 1	Pioneer						
102	SEQ. ID. No. 2	Pioneer						
103	SEQ. ID. No. 3	16 kD E_2 enzyme	-	-	-	+	+	-
107	SEQ. ID. No. 4	Peroxidase	-	-	-	-	-	-
108	SEQ. ID. No. 5	Pioneer	-	-	-	-	-	-
110	SEQ. ID. No. 6	Pioneer						
111	SEQ. ID. No. 7	Pioneer						
112	SEQ. ID. No. 8	Pioneer						
113	SEQ. ID. No. 9	Pioneer	-	-	-	-	-	+
114	SEQ. ID. No. 10	Pioneer	+	-	+	+	+	-
115	SEQ. ID. No. 11	Pioneer	+	-	+	+	+	-
117	SEQ. ID. No. 12	RNA pol II Heptamer repeat						
118	SEQ. ID. No. 13	Pioneer	-	-	-	-	-	-
119	SEQ. ID. No. 14	Pioneer	-	-	-	-	-	-

[1]RNA samples from the tissues indicated (G: gall; D: RNA isolated from cultured, uninfected roots, and used as driver for the subtractive cloning; L: leaf; H: hypocotyl; A: cotyledons plus apex; R: primary root from young seedlings) were probed with anti-sense probes from the cDNA clones: + indicates a signal was detected, - indicates no signal was detected, no entry indicates that the clone was not tested.

[2]Putative identity of partial cDNA clones based on DNA or deduced amino acid homology with sequences in GenBank or PIR. Clones with no meaningful homology were termed pioneers.

122	SEQ. ID. No. 15	Extensin-like pioneer	-	-	-	-	-	-
124	SEQ. ID. No. 16	Pioneer	+	?	-	-	-	-
131	SEQ. ID. No. 17	Receptor kinase homologue	+	-	-	-	-	-
132	SEQ. ID. No. 18	Anti-integral membrane protein	+	-	-	+	-	-
133	SEQ. ID. No. 19	Zea repetitive element/cyclophylin 3'	+	-	+	+	+	+
134	SEQ. ID. No. 20	Pioneer	-	-	-	+	-	-
136	SEQ. ID. No. 21	16 kD E_2 enzyme						
137	SEQ. ID. No. 22	Pioneer	-	-	-	+	+	-
139	SEQ. ID. No. 23	Pioneer	+	-	+	-	-	+
140	SEQ. ID. No. 24	Pioneer	+	-	+	-	-	+
141	SEQ. ID. No. 25	Pioneer	+	-	-	+	+	-
142	SEQ. ID. No. 26	anti-Ef-3	-	-	-	-	+	-
144	SEQ. ID. No. 27	Ribosomal protein L38						
146	SEQ. ID. No. 28	Pioneer						
147	SEQ. ID. No. 29	Pioneer						
148	SEQ. ID. No. 30	Pioneer						
149	SEQ. ID. No. 31	Pioneer						
151	SEQ. ID. No. 32	Pioneer						
152	SEQ. ID. No. 33	Pioneer						
153	SEQ. ID. No. 34	Anti-ripening associated membrane prot						

154	SEQ. ID. No. 35	Pioneer						
155	SEQ. ID. No. 36	Pioneer						
156	SEQ. ID. No. 37	Pioneer						
157	SEQ. ID. No. 38	Pioneer						
161	SEQ. ID. No. 39	Pioneer	-	-	-	-	-	-
163	SEQ. ID. No. 40	16 kD E_2 enzyme	-	-	-	+	+	-
164	SEQ. ID. No. 41	Pioneer	-	-	-	-	-	+
165	SEQ. ID. No. 42	Pioneer	-	-	+	-	-	-
166	SEQ. ID. No. 43	Pioneer	-	-	+	-	+	-
168	SEQ. ID. No. 44	Mucin						
169	SEQ. ID. No. 45	Novel 16 kD E_2 enzyme						
172	SEQ. ID. No. 46	L38 ribosomal protein						
173	SEQ. ID. No. 47	Pioneer	+	+	+	-	-	+
175	SEQ. ID. No. 48	Pioneer						
176	SEQ. ID. No. 49	Pioneer						
177	SEQ. ID. No. 50	Proline-rich wall protein						
178	SEQ. ID. No. 51	Pioneer						
179	SEQ. ID. No. 52	Pioneer						
181	SEQ. ID. No. 53	Transmembrane turgor-responsive prot						
182	SEQ. ID. No. 54	Pioneer						
183	SEQ. ID. No. 55	Pioneer						

187	SEQ. ID. No. 56	Pioneer						
197	SEQ. ID. No. 57	Pioneer	-	-	-	-	-	-
198	SEQ. ID. No. 58	Pioneer						
199	SEQ. ID. No. 59	anti-Ala tRNA synthase	-	-	-	-	+	-
201	SEQ. ID. No. 60	Pioneer						
203	SEQ. ID. No. 61	Pioneer	-	-	-	-	-	-
205	SEQ. ID. No. 62	Pioneer						
207	SEQ. ID. No. 63	Pioneer	-	-	-	-	-	-
208	SEQ. ID. No. 64	Pioneer	-	-	-	-	-	-
209	SEQ. ID. No. 65	Pioneer						
210	SEQ. ID. No. 66	Pioneer	-	-	-	-	+	-
212	SEQ. ID. No. 67	Pioneer	-	-	-	-	+	-
214	SEQ. ID. No. 68	Pioneer	-	-	-	-	-	-
215	SEQ. ID. No. 69	Zn-finger domain	-	-	-	-	+	-
216	SEQ. ID. No. 70	Pioneer	-	-	-	-	-	-
217	SEQ. ID. No. 71	Laminin B receptor	+	-	+	-	-	+
218	SEQ. ID. No. 72	Pioneer						
220	SEQ. ID. No. 73	anti-PEP-carboxylase	-	-	-	-	-	-
221	SEQ. ID. No. 74	Pioneer	-	-	+	-	-	-
222	SEQ. ID. No. 75	Pioneer	-	-	-	-	-	-
223	SEQ. ID. No. 76	Pioneer	-	-	-	-	-	-
224	SEQ. ID. No. 77	Pioneer	-	-	-	-	-	-

226	SEQ. ID. No. 78	Proton ATPase	-	-	-	+	-	-
227	SEQ. ID. No. 79							
228	SEQ. ID. No. 80							
230	SEQ. ID. No. 81							
231	SEQ. ID. No. 82							
232	SEQ. ID. No. 83							
233	SEQ. ID. No. 84							
234	SEQ. ID. No. 85		+	?	-	+	+	+
236	SEQ. ID. No. 86							
239	SEQ. ID. No. 87	eF Ile 5'UTR	-	-	-	+	+	-
240	SEQ. ID. No. 88	Pioneer	-	-	-	+	+	-
241	SEQ. ID. No. 89	Pioneer						
244	SEQ. ID. No. 90	Pioneer	-	-	+	-	+	-
246	SEQ. ID. No. 91	Pioneer						
247	SEQ. ID. No. 92	Pioneer						
249	SEQ. ID. No. 93	Tob RB7-5A homologue						
250	SEQ. ID. No. 94	Pioneer						
252	SEQ. ID. No. 95	Pioneer	+	-	-	+	+	+
255	SEQ. ID. No. 96							
256	SEQ. ID. No. 97	Pioneer						
263	SEQ. ID. No. 98	Pioneer	-	-	-	+	+	+
264	SEQ. ID. No. 99	Pioneer						

265	SEQ. ID. No. 100	anti-Tnt1-94 transposon	-	-	-	+	+	+
266	SEQ. ID. No. 101	Pioneer						
275	SEQ. ID. No. 102	Pioneer	-	-	-	+	+	-
277	SEQ. ID. No. 103	Pioneer						
279	SEQ. ID. No. 104	Pioneer	-	-	-	-	-	+
280	SEQ. ID. No. 105	Myb DNA-binding site	-	-	-	+	+	-
288	SEQ. ID. No. 106	Pioneer						
289	SEQ. ID. No. 107	Pioneer						
291	SEQ. ID. No. 108	Pioneer						
L23762	SEQ. ID. No. 109							

Only one clone (DB#173) produced a signal in the RNA from mature roots. This is important because mature root was the source of the RNA used as driver in construction of the subtractive library, and provides strong evidence that the subtraction was effective. Fifteen of the cDNA clones detected transcripts in seedling root (Table 1), and presumably encode functions associated with young, expanding roots. Three of these appeared to be root-specific.

Despite the fact that only cDNA synthesized from giant cell mRNA was exposed to the vector thereby ensuring that all clones in the bank must encode giant cell transcripts, most probes also failed to detect transcripts in gall RNA. Although this is partly due to giant cells representing only a small fraction of the total mass of the gall (it was not technically feasible to collect the numbers of giant cells required to isolate sufficient RNA for blot analysis), it also suggests that the clones in the bank do not encode abundant transcripts. Ultimately, the (elevated) presence in giant cells of transcripts defined by each clone in the bank can be confirmed using, for instance, *in situ* hybridization.

Although different clones reveal a range of expression patterns, many detected transcripts in RNA isolated from hypocotyls and/or cotyledon plus apex tissue, generally at levels much higher than in uninfected seedling root. Ten cDNA clones detected a signal in leaf RNA. Overall, these results give a picture of giant cells sharing transcripts with actively dividing and expanding tissues, and also non-root tissues.

DNA sequencing

Partial sequences of each clone listed in Table 1, above, are provided in the Sequence Listing, below. The Sequence Listing also includes the complete sequence of one clone, SEQ. ID. No. 109, which encodes a ubiquiitin carrier protein. Reflective of the directional nature of

the cloning, each sequence began with a poly-T tract (ranging in length from 4 to 75 residues), corresponding to the poly-A tail of the transcript. Each sequence was read only as far as the first ambiguity, including potential compressions. Thus, although the sequences represent readings from one strand only, we believe the degree of accuracy to be high. The presence of a long oligomeric tail rendered some clones unsequencable. Four independent rRNA clones from the same bank also were determined. The sequences (not shown) corresponded exactly to those published for tomato (Kiss *et al. Nucl. Acids Res.* 17:796 (1989)). This suggests also that the number of PCR-introduced artifacts in the bank is low.

Sequences were compared to others in the public domain DNA and protein databanks using the BlastN and BlastX algorithms (Altschul *et al. J. Mol. Biol.* 215:403-410 (1990)). With some exceptions noted below, only those database matches involving homology with the correct strand and in the correct part of the matching gene (i.e., the 3'-end) were considered, and a score of at least 100 was chosen as indicating a potentially valid homology. Most of the cDNA sequences failed these tests, and are listed as "Pioneers" in Table 1. Four clones were determined to share sequences with genes previously cloned in tomato, all other non-pioneers shared sequences with sequences from other species.

By isolating and characterizing full length cDNA clones, including *in situ* localization to giant cells the identity of the DB#103 transcript was confirmed as encoding an E_2 enzyme, a key component of the protein ubiquitination pathway.

The DB#163 cDNA is identical with the DB#103 sequence, but has an additional 19 residues immediately before the poly-A tail. Because the gene encoding these transcripts, *LeUBC10*, appears to be unique, the different 3'-ends might arise by differential RNA processing.

Computer translation of the DB#117 cDNA revealed a hypothetical protein with multiple contiguous repeats of a seven amino acid motif, shown aligned in Figure 2, and terminating with a stop codon 47 bp 5' from the poly-A tail. This motif is strikingly similar to the motif TSPSYSP, a structure diagnostic for the carboxy terminal domain (CTD) of the large subunit of RNA polymerase II. *Arabidopsis* has 40 copies of this repeat (Dietrich *et al. Plant Mol. Biol.* 15:207-223 (1990)) and *C. elegans* has 42 (Bird and Riddle *Molec. Cell. Biol.* 9:4119-4130 (1989). Although not previously cloned from tomato, it seems likely that DB#117 encodes this gene. Southern blotting (not shown) suggests that the DB#117 region is unique.

BlastX analysis revealed significant homologies between the inferred DB#280 product and different members of the *myb* gene family (Fig. 3). Homology is highest with the DNA binding domain of the petunia *myb Ph3* gene product, although multiple alignment with Mybs from other plants and vertebrates revealed that this homology extends further. As nuclear transcription regulators, members of the Myb family play pivotal roles in the regulation of cellular proliferation. Through interactions with other trans-activators (e.g., members of the Ets family) Myb proteins effect growth control and oncogenesis.

A BlastN search revealed striking homology between the DB#226 sequence and the 3'-end of the *pma4*-encoded isoform (Moriau *et al. Plant Molec. Biol.* 21:955-963 (1993)) of a plasmalemma H⁺ATPase from *Nicotiana plumbaginifolia* (Fig. 4). The DB#226-gene appears to be different from those encoding two previously cloned tomato isoforms (Ewing *et al. Plant Physiol.* 94:1847-1881 (1990)). The high degree of homology between the 3' untranslated regions (UTR) of these genes (the tobacco stop codon, and presumably also the DB#226 terminator, is

a further 60 residues 5') might indicate a biological role for this part of the sequence.

Other sequences in the giant cell cDNA bank, including a number of the pioneer clones, encode recognizable structural motifs. For example, part of the DB#215 sequence specifies a zinc finger domain. Additional homologies have been observed in the UTRs of some genes. The 3'-UTR of DB#239 contains a $(GCC)_5$ element previously noted in the 5'-UTR of human general transcription factor TFIIE (Sumimoto *et al. Nature* 354:401-404 (1991); sequences such as these may play a role in translational regulation.

Four clones in the cDNA bank (DB#142, DB#199, DB#220, DB#265) have high degrees of homology with sequences in GenBank (Blast scores of 246, 499, 806 and 173 respectively) but to the anti-sense strand. These sequences terminate with a poly-A tail, suggesting that they do not represent artifactuary cloned sequences. Significantly, when used as probes in the dot blot assay, DB#142, DB#199, and DB#265 detected transcripts in plant tissues (Table 1). The DB#265 transcript, which encodes a sequence with anti-sense homology to the tobacco retroviral-like transposon Tnt 1-94 (Grandbastien *et al. Nature* 337:376-380 (1989)), and also the *Arabidopsis* copia-like element (Voytas and Ausubel *Nature* 336:242-244 (1989)), appears to be particularly abundant in seedling root tissue.

The cDNA clone DB#249 as a query revealed that its inferred product shares homology with that of the RB7-5A gene from tobacco (Yamamoto *et al. Nuc. Acids Res. 18:7449* (1990)). Significantly, this gene is strongly up-regulated in nematode-induced, tobacco giant cells.

Taken together, these data show the subtracted library contains bona fide cDNA inserts with a low level of contamination by high copy or nematode sequences, as well as a high degree of complexity.

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

(ii) TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO

(iii) NUMBER OF SEQUENCES: 114

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Robbins, Berliner & Carson
(B) STREET: 201 N. Figueroa Street, 5th Floor
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: US
(F) ZIP: 90012-2628

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Berliner, Robert
(B) REGISTRATION NUMBER: 20,121
(C) REFERENCE/DOCKET NUMBER: 5555-316

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (213) 977-1001
(B) TELEFAX: (213) 977-1003

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..210
(D) OTHER INFORMATION: /standard_name= "DB# 101"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACACGATCAC ATACCAGAGG GCAGACAACC AAGCTGAGAG GTCAAGTGGG TCTGGGAGTT 60

CAATTTCCAA GTCTATGAAA ACCAGTTCTT CAACAAGTTC CGGTGCTGAT CCTTCATTGG 120

TTCAAGCATC ATTGTTAGAT AGTATATTGA GGGAGAACCT CTTGTGATCT GGAGAAAGTA 180

ACCTATTACA GTATTTTGTA CCTCTTACGT 210

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..211
(D) OTHER INFORMATION: /standard_name= "DB# 102"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CATAAACCTG TTTTTCTCTT TCCCCCTTAT GATGAATCCA GTCTATGAAG TAATGGAAAG 60

GAGATTCTGG GAAGGCAGGT ACTGTGTGTG GTTGAGATGG CTTGTGGTTT TAGCAGTGAC 120

TTTTGTTGCA TTGGCGGTGC CCAATTGTTG CTGATTCTTT CACTTGTTGG GAGCAGTGTG 180

TGCATTGTTT TGGGATTTGT GTTGCCTTCT T 211

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..257
(D) OTHER INFORMATION: /standard_name= "DB# 103"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AACTGGCAAA CAAAGTAGAA TTACATTGCA GTTTCTCCCT TACTAGTCAT CAAATAAATA 60

TTCACAAATT GAAAACAGCT GTTCCCTTAA CAACCCTCAT GAAGGGAGAT TAAGAAGTAA 120

CTAAGTTCTT TCACGGAATT TATTCATTCA CCCCAAGCAC ATAAGACATT GCTGTTACAA 180

AGTCCCAGAC ATGCCTGGAG ACATTTTGCG CATCATCCCA TTGCATATTT CTGAGTCTAG 240

CTACGAGCAG TGGTTTC 257

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..249
(D) OTHER INFORMATION: /standard_name= "DB# 107"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGGTCAAAT TTGGAATTGC AGTTTGCTCA CTTGGCCCTC CTGCTGATCC ATCTAGCAAC 60

ACTGAACCAT CACACCCCTG AACAAAGCAA TCGTGGAAAT GAAGACGAAG TAAGCCAGCA 120

GCTTGGCCAA CATCATCCTT GATTTGTTTT TGAAGCCTGT TTCTAATAAT GGATTCAAGT 180

TGAGGACAAC TAGATTGATA AATGACCATG AGACCTTAGT TAGCAGCCTT GAGCTTCCGA 240

TCAAGATTT 249

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..132
(D) OTHER INFORMATION: /standard_name= "DB# 108"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGATTACTG AGGTGGTTTT GGATCTTTCT TCCGGCCTTT CGCTATATAC ACAAGATAGG 60

ACAATGATCA GTAGTTGTTT GTTGTTGTCC TTTGTCCTGA GACTTTTGTC ATGTTAATGG 120

GGTTTCCAAT GC 132

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..207
(D) OTHER INFORMATION: /standard_name= "DB# 110"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCAGTCCCT TTGGGTGTCA CAATTTTCTC AGCACTTGAA CTCAAGCCAT TAGGATCAAT 60

GTTATTCCCT CTCTTAATAG CTGGTAGTCT TGGCGACTTC ATTTTGTGGT CGCTGCTTTA 120

GATCTGTTAC ATATTAGCGG CTTTTCTTTT GTAGCATCTC AGTTAGAAAG TACTGGACGT 180

GCCTTTTCTT TGCGCACGAT AAACACG 207

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..256
(D) OTHER INFORMATION: /standard_name= "DB# 111"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAATTACACC CATTTTATCA ACCTTGGAGT AAATCTTACC AGCACTAAAC TGGCTTACAA 60

TGCCATGGGC AGTTCGCTCA ATAACAATTC ATCTAAAACA TTTTGGAAGG CACTGTGCTA 120

ATGTTTCTAA CACATAAAAT TGAATCTAAG GTCCAAAATT TAGTTTTCAT TACAGAGGCA 180

GCCAAGAATG CAAACAACTA CCAACCATGC ATTTGCATGA CTGTGGATCT TCAACTTCAT 240

CTCACAACTA ACGCAT 256

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..179
(D) OTHER INFORMATION: /standard_name= "DB# 112"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTATGTTGT ACGCTGCTGT TGAAGTTGAA GATCTGAAGA TGCGTTTGCT GCTGTTGGAA 60

GTTAAATCAT TTTGGTCACA CTGTTGGGTT GTTCCTGTTA CATTTGGAAA CACTCAACTT 120

TTAACTCCTA AACTTGTTGC TGTTGCTTGT CTGAATCTGT CGTGTGCATC ATTAACACA 179

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..210
(D) OTHER INFORMATION: /standard_name= "DB# 113"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTAAAAGCT AGTCTTTCTT AGGTTCACAT AGCAGTTACT TCCAAAAGTT AAAACATAAA 60

TCAAAATTAT CCCATTACAT CATTTAACTG AAGGGAGATG CAAATCAAAA AGCTCTAATG 120

CCATATGTCT TCTACCAGCA CCAAATGTAG AGGTCCTCGT AGAAACTCGT ATTCAAGATT 180

TTTAACGGTA CTTGATGAAG CCAATTCCTT 210

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..110
(D) OTHER INFORMATION: /standard_name= "DB# 114"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGGAGGTTTA TCTGATACAG TTGACTTGAA ATATGGCATA TTGGGTCTTA AGCCAACATC 60

TGCTTCAGTC ATCTTATCCA AAACTGACTT GACAAGTTCA ACATTTTCCG 110

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION: 1..223
(D) OTHER INFORMATION: /standard_name= "DB# 115"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCTCAACT AGTCGAGCTA GTAAGAAGAG AGATTATAAT TGTAAAATCA CTCACCAATA 60

CCTGCATTAT ACACACCAAA TGTAAGGCAA ATATAAGAAT TCACTTATTT AGCTTCTTCT 120

GGATCTACTT TGATAGAAAG CGCAGTGGTA CATGGTGGAT GAGCAAGACG AACAATACTT 180

CAAAGAAGAC CATCATGAAA GTTGTTGACA TGCTTTAATC AGT 223

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..279
(D) OTHER INFORMATION: /standard_name= "DB# 117"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTAACCACCG TCGTATTTTC CGCCGATACC CATCGTCGTA GCTGGGCTTA TAACCTGTCG 60

TAGCTTGGCT TGTAATTGTC ATAGCTAGGC TTGTAACTGT CGTAGCTTGG CTTGTAATTG 120

TCATAGCTAG GCTTGTAACT GTCGTAGCTT GGCTTGTATC CGCTGTCGTA GCTAGGCTTT 180

TTGTAACCAT TGTCGTAGCT GGGCTTGTAT CCGCTGTCGT AGCTGGGCTT TTTGTAACTA 240

TTGTCATAGC TGGGCTTGTA GCTGTCTGAG CTGGGCTTT 279

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..267
(C) OTHER INFORMATION: /standard_name= "DB# 118"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAGTGAAAT CTTCAAAATA GCAGTAAAAT TGGTACCTTC ACTATAACTG GTGTTTCATA 60

TTTTTCTTAG CTAGAATGCA GTTGATTTGT TACAACAAAT ACTGAGTTAA TGAGGCCTTG 120

TAGTAGTAAG TTGGGACCAA ATTGGATTTC TCATCATTAG ATTGTTTGTC CAGTTACTAC 180

CTTCAGGTAG ACAAATATAC TTAGTAAGAG GAGAAACCAA TGGAAGAGAA GGTGATTGTA 240

GCCATGGTTA GGGCATGTTT CTTGGCT 267

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..199
(D) OTHER INFORMATION: /standard_name= "DB# 119"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACCTACCACC TCCCACCGGC AATAGGTACA GTCCACCAAG GCTAGGACAG ATGGAAATAA 60

CTACCTAGTG TTTTCTTGTC TCCGCTAGAA ACAAAATTAG CTAGTTTTCA TCTTCAAGAT 120

CCAAACAAAG GCAGTAAGCA ACTAAGCCAC AACTGAACAT ATCTGAGATA TCTCACTATG 180

TCAGCCTTAT CTTCCTGGT 199

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..303
(D) OTHER INFORMATION: /standard_name= "DB# 122"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGGGTGAGGT GGTATTTGAG GATTGGGGTT TTGAGGAGGT GGTGGGATGT GGTAAGGGGT 60

TGAGGCATAC TAAGGATTTT GTGCAGTCAA GTCTATTACT GAGTGATTCT AACCAGGAGT 120

GGATAGTGCG TTCTTAGCCT ATTCTATGTT TGAAGAGGGA AAGTGTTGTA GAGGCCTTCC 180

ATCAGTATTA GTGTTGGCAG TAAAACCTAA TGGAGGCAGA TCCTGTCTCT TTGCATTTCC 240

ATTCTCATCT CAGTGATCTG CTGCATTAAC TGTATAATCT GTTCATTCTG ATCTGCTATA 300

GTG 303

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..196
(D) OTHER INFORMATION: /standard_name= "DB# 124"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGAGGATA TCCATTTGTG AGCAAAGCAT CAAACTTACA ATTGATTACA TAAGAAGCTA 60

TGTGTCAAAC TGCTGAATCT AAGAAAGTGG TACTCGATTG GGAGTTGAGG ATATGACAAT 120

GAATTAAACC TGTTAGATGT AAATCTGCCT AGTAATTCTA TGAATTACCG ATAGTTTGAA 180

TTGGACAAGT TAGACT 196

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..272
(D) OTHER INFORMATION: /standard_name= "DB# 131"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAAGGCTTCA CACTGAGCCA TGAAGTTCTT AGAAGTAGCC CCTTGTTGTT CAATGTTTAT 60

CACCTTCACC GCAACCATAC ATTCACCTGG ATCAAGTACC CCTTTGTAAA CAGAAATAAA 120

GCTACCATTT CCAATCAAAT TGGCAGAAGA GAATCCATTT GTCGCTCTAT ATAGGCTCTC 180

ATAAGTAACC GGTGAAGATG TTAAAGAAGG ATCTCCCTTG CCTTCCTTAA CCGAATGATT 240

ATGACTAAGC ATGATGAAAC CATGCACAGT CC 272

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..164
(D) OTHER INFORMATION: /standard_name= "DB# 132"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGTCATGAC CGAATTGGCT CTAATTGGGG CTGATATTCA AGAGGTTATT GGAAGTGCTA 60

TTGCTATAAA GATTTTGAGT CGAGGGTTCT TGCCTCTATG GTCTGGTGTT GTCATCACTG 120

CTCTTGATTG CTTTGTATTC TTATTTCTTG AGAACTATGG ATGA 164

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(xi) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..348
(C) OTHER INFORMATION: /standard_name= "DB# 133"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAAGTCTA TGAGTATCTT ATTTAATTGT AGTCTTAAGA TTAAACATAA ACTGGTGGTG 60

CACCAGCTGG TCGTGTGGTG AACGAGACTT TGGATTTGTC CATTATGCAG AAAGGTCGAG 120

CGCTCTGAAA GCTGTCAAAG ACACTGAAAC ATATGAAGTA AATGGTCAGA TGTTAGAAGT 180

AGTTCTTGCA AAGCCTCAGA CTGAAAAGAA GTTTGATGCA GCTAGTCCTC ACATGCGATG 240

CCACATCATA TTATATTCCC ATCCAGGCTA TGGTGACTTC CGATGACCGA TGTCACCTAT 300

CTGCTGGTAT GGTCGTCGTC GTCGTCGTCG TCCGCGTCGT CACACACC 348

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..239
(D) OTHER INFORMATION: /standard_name= "DB# 134"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AACCCATCAA AAAGTGTATT TATATCTCAG TGAACATATG TTCAGCACTC GTGCTGTCTG 60

ATCTAGGGCC AAAACTGGCA CAGGTACAAC CTGCAATACC TCATTACAAC ATTTGAGAAA 120

TGAGCAAATA ATACTTCCAC ATTCAGCATA AACAAAAGTT ATCTTGACGT TGATCTGTTT 180

AAGATGAGAT GATGATCTGT TTTTCTCAGC CAATAGTGCT CAGCATATCT TCTTCATCA 239

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..255
(D) OTHER INFORMATION: /standard_name= "DB# 136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCAAACAAA GTAGAATTAC ATTGCAGTTT CTCCCTTACT AGTCATCAAA TAAATATTCA 60

CAAATTGAAA ACAGCTGTTC CCTTAACAAC CCTCATGAAG GGAGATTAAG AAGTAACTAA 120

GTTCTTTCAC GGAATTTATT CATTCACCCC AAGCACAATA AGACATTGCT GTTACAAAAG 180

TCCCAGACGT GCCTGGAGAC AATTTTGCGC ATCATCCCAT TGCATATTTC TGAGTCCAGC 240

ATCGAGCAGT GGTTC 255

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..283
(D) OTHER INFORMATION: /standard_name= "DB# 137"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATAATCCAA TAAAATACAG ATTGGAAGTT ACATTACAAT CCCAAATGAC ATGATATTAT 60

ACGTTCATCA AACAATCTAT CCACAAGAGA AAACAACCAA AAGCCAAGAA TAAATGGAAA 120

AAGTAGCTAG GTACTCCATT AGCGAAGTAG TAATAATATG GTCTTCAAAT ATCCACCATA 180

TGATGATCCA CTTGGTGAGG ACCAAATAGC ATAAATGATA CCAGGTAGCT ACCAAAGAGA 240

GTCAGCAAAC TGATGTTTTT GGCTATGGAA TCATGCTTGG AAT 283

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..243
(D) OTHER INFORMATION: /standard_name= "DB# 139"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAATTGTC CTACAACTGC ATTGCACAGA AGAGTACAAT TTTTTTTCTC TGAAATTTAT 60

TACACCTCAA GTAGTCCAAG TCCAGGCAGG ATCATCAGAT GTACAAAGAT TTGCTCAGTT 120

TTGTTCCTCC TAATCAATTC AAAGGATCTA ACTCAAAACT TGGCGTTGCA ATAGATAAAT 180

GCTGCTGGAT AATTAGGATA CAACATATCT AGTGTAATCC CACATAGGTC TGGAAGGGTG 240

GTT 243

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..223
(D) OTHER INFORMATION: /standard_name= "DB# 140"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GACTTGAGAA CGTTAATATA AAAGGTAAAT GATTGTGGTT AAAATAATTT TACGTCTGGA 60

TAGCTTTTTA TACAAGATTT TGGAGTTGCT TCTCCTTAAA TCATATTAAG GAAAGACACA 120

CCTCCAAAAC ATTCTCTTGG AAGAAATACC AATTGAAACA CATTACACAT ACTGAGTTGA 180

GGGTCTTGTA ATAGGCATCA GTTAGGGTCA GGATAACGAG TTT 223

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..163
(D) OTHER INFORMATION: /standard_name= "DB# 141"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTTATTTAT GTCTGGTGTT TCTTCTAAAC CTTGGGTACT TGCTGTAACC CAGTACGGCA 60

GTACCTGCAG TTTTTCTTTA TCATATGATC TTATTATGTG GGACAGCAAA CGGCCAGCCG 120

ACCGAAGCCG GCGCTTCAAC CAGGATCATC TATGGAGGAA TCT 163

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..206
(D) OTHER INFORMATION: /standard_name= "DB# 142"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTCAGCCTA CTCTATTGTT GTTGGATGAA CCTACAAATC ATCTTGACCT TCGGGCTGTT 60

CTATGGTTAG AGGAGTACTT GTGCAGATGG AAGAAAACTT TGGTCGTTGT TTCGCATGAT 120

CGAGACTTTC TGAACACTGT TTGCGGTGAG ATTATTCATC TCCATGACAT GAAACTACAC 180

TTCTATCGTG GTAACTTTGA GATTTT 206

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..309
(D) OTHER INFORMATION: /standard_name= "DB# 144"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGGGGGCAA CACAATATCT AGAATGAACA AAACTTTAGA TATTCGACAG GATAAGAAAA 60

TGGTAAAGGA ACATAATAGT TCTACGAATT CTCAAGTATC TTCTAATCAT CTAGGGGGAA 120

GGGGCACATT AACTCTTCCA TCTTCAAGGT CTTGGACGCT CAAACCTGGA GGAAGTGACT 180

GCTTCAACTT GTCAGCCTTC TCAAAGTCCA GCACACAGAG TGTGTAAAGG TACTTGGAGC 240

CAGCGACCTT GAACTTACCA TATCCTTGTT CTCTGATCTG CAGTCGTGCA TCCTCCTCCT 300

TGCTGTAGG 309

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..292
(D) OTHER INFORMATION: /standard_name= "DB# 146"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGTGTGAGTT AGTTTTTTGT GGTTTTCATG AATGCCGTGT CAAGGAGACC TTAGATTTGT 60

GTTTTGACAG TTTCATCGAG TCTAAAGCAT CGAGTATATT GATTTGCTTA TGCGGTTTGT 120

GTGTACCGGA TTCCGAACGA ATCCTGAGGG TCCTCTTGAT GTTTTGGAAG TTGGCTGATT 180

TTTCTGGTGC CTGAATCTAG TGTGTCTCGC GATCTCGAGC CTCATTGTTG CGAGGTAATG 240

TTCGCTTCGC GAAGGGGTCA AGTTCCTGAT CTCACGTACA CAAGAAGGAC CT 292

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..176
(D) OTHER INFORMATION: /standard_name= "DB# 147"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCGCCCTAG GCCACCATCC TTCTTAAAGT AAAGGAAGAA AAGAGGAAGA AGATTGCTAA 60

GAACTTGAAG AAGTACAGCA AGAAGTATGA AGCAGAGGAT CAGGATGTTT CATTGCTGTT 120

GAGCGAGCAA GACCGTGAGA AGCGAAAGAA GCTGAAAGAG ATGGGAGCAT GGATTA 176

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..184
(D) OTHER INFORMATION: /standard_name= "DB# 148"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAGATGATTA AGCTAAATAT CAAATAGAAA CCAAATCCAT AGGACATATA TCTTTTTAAC 60

AGCAATAATT CCAATCTAAC AGATGAGAGG TAATATTCCA GAAAAAAATA TTCGAAACTT 120

CGATTCATCA GCGAAATGAA AGACATCAAA CGAAACAGTG TCAAAACTGC TTCTTTAGAA 180

ACGT 184

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..325
(D) OTHER INFORMATION: /standard_name= "DB# 149"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ACCGTTCATT TTGGAATCGT AGCACAAAAC CTTCTTTGGA TCTCGCGAAG GAGCTCCTAG 60

ATCTTTTTAG TGCAAATAAA ATGGCGAAAC GCTTTTTTTT TCACAAACAG CGGATCAGAA 120

GCCAATGACA CACAGGTGAA ACTGGTATGG TATTACACAT GCACTCGGCC AGACAAAAAG 180

AAATTTATTG CTCGAACAAA ATCATACCAC GGATCCACCT CTCATTTCCG CTAGTCTCTC 240

TGTCTTCCTG CACTACATCA GCAATTCGAT CTACCAGCTC CGTTTGTCTG CATACTGACT 300

GCCCTATTTG GCGCTTCATC AGCCA 325

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..249
(D) OTHER INFORMATION: /standard_name= "DB# 151"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGACTACAAA CTTTTGATGC TCTATTTCCC TTGTAAGATA CTTATAAGAA CTACAATGTC 60

TTAACAAGGA CAGTTTTGTT CAAACTAAAT ATCCTTGATC CATCTGTCAT GAAAGGATCT 120

GAAAATACCA TTGATTCAGC AAAAACTACA CAAAGGACAT ATACTAGCAA TAAAAGTTGC 180

AGGAACACAT ACTGCCGTCA AAGAGAGTTC AGGCCAGCGA CATTGTTCTA TTAATCCTAC 240

TGGTATCCC 249

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..211
(D) OTHER INFORMATION: /standard_name= "DB# 152"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AACTTAAATG AACTTCTAGC TTAAGATAAA CAGTTGAACA TCACCAGATA ACGAAAATAC 60

CGGCGAAACG ATAGGAGTTT AGTCAAGCCA AAAGTATTAT TATGGATAGC AAATAATCAG 120

GACAGTGATC TACTACTATG TCTTTGCAAG AAAAAACTGT TGCTACAAAC TATAATTACT 180

AACCGGTCTA CATGTAGGGT TGATAGGCTG T 211

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..302
(C) OTHER INFORMATION: /standard_name= "DB# 153"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTGGTATGA TCTTTGCTTT GGTTTACTGT ACTGCTGGTA TCTCAGGAGG ACACATTAAT 60

CCAGCTGTGA CATTTGGTTT GTTCTTGGCA AGGAAGTTGT CATTAACAAG GGCAGTGTTT 120

TATATAGTGA TGCAGTGTCT TGGTGCTATC TGTGGTGCTG GTGTTGTGAA GGGTTTTATG 180

GTTGGACCCT ATGAGAGACT TGGTGGTGGT GCTAATGTTG TTAATCCTGG TTACACCAAA 240

GGTGATGGAC TTGGTGCTGA GATTATTGGT ACTTTGTCCT TGTTTACACT GTTTTCTCTG 300

CC 302

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..243
(D) OTHER INFORMATION: /standard_name= "DB# 154"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGATTAGGTG ATAGATATGA ACCCTAGAAA TAGGGGATTT TTGGCTAATT CAATTGAAAG 60

ATTGATTAGA GATCAAATTA AGGAGATCGG AGTATGTAAG GCAAGCAGTG CAAGAGGACA 120

ATGGTGGAAA CTATGCAAAG GCATTTCCGT TGTATATGAA TGCATCGGAG TACTTCAAGA 180

CCCATTTGAA GTACGAGAAG AATCCTAAGA TAAAGGAGGC AATTACCCAG AAATTTACTG 240

AGT 243

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..272
(D) OTHER INFORMATION: /standard_name= "DB# 155"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGCTGATTA AACCTTCCAG TGATGGAAAT GCTGGTCCTG AGTTGGTTAA AGGGAGTAGA 60

AAGTCACAGA TGCGAGGAAG ATGGAGAGGG ATTGACCCAA TATTATTTTA CCACGAGGAG 120

ACAACAGTGG GTCAGATAAA GGCCTTCTAT GGCATTAAGG AATCCTTTCC ATTCAAAGGT 180

CATTTGATTG TGAGGAATAC TGATATCGAC CATGTGAAAA GAGTTTATTA TGTATCTAAA 240

TCTGTGAAAG AAGTTCTTAA ACTCAATTTT GT 272

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..279
(D) OTHER INFORMATION: /standard_name= "DB# 156"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACCAGAAATG CAGATTGGAT AGAGATGATT CCACAAAGGG AATCTTAATT GAAACAAGAA 60

GATATCCTGT GAATATATTT ACAGATTGAG ATAAGACTTC TATAAAACCT CAAAATTCCT 120

CAATCATCTG ACACCTAGCT TACTATTTTA CCTGGTTCTG TCAGCCTATT TATACCAACA 180

AGACCTACAT CTTAAGAAAT TAGAGACAGA TCCTAATAAT TCATCTTCAT ACATGTTATT 240

GACATTGCCG CCATCTCGTG ATTTATCCAA GCAGCAACC 279

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..183
(D) OTHER INFORMATION: /standard_name= "DB# 157"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCTGGTAAC AGAATGAACC AAGGAAGAGA GCAATTTCCA GTCCATAAAT AAAACTAGCA 60

TCAAAATGCC CAACAGCAGA GACCCTAGCT GCCAATAAGA CATCAATTTT CTAATGTTTT 120

GCCTTAACTA AATGTGCCTT TCAGCTGTGA CTTCAAAAAT ACGAGACTCA GGTTTCTTAT 180

GGG 183

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..290
(D) OTHER INFORMATION: /standard_name= "DB# 161"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGAGAGAGAT CCCGGTCTAC AACATCACAT TAGAGAGGTA TTCTCAAATA TACAAAACAG 60

AAACACCCCT CTATCTCTTG AAAGTTTAGC AAGTTTGTTA AATTGCAAGA ATCAGTGCAT 120

GCTTGTTGAT AAGTCCTTGA AGATAGCTGC TCAACTTGCT GTTCAACTTG GGGGTAGATA 180

TTAGACATTA TATAGCCTCA TTTCCTCTTC GGTGCAATAG TTAGTAACTC AAAGCTCCTA 240

AGAGCATCAT CCCTACCCCT CTAGTTGGCA GGTAGCCGCG GTAAGAGTAG 290

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..279
(D) OTHER INFORMATION: /standard_name= "DB# 163"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGGAAAGGC GAATGTCAAA CTGGCAAACA AAGTAGAATT ACATTGCAGT TTCTCCCTTA 60

CTAGTCATCA AATAAATATT CACAAATTGA AAACAGCTGT TCCCTTAACA ACCCTCGATG 120

AAGGGAGATT AAGAAGTAAC TAAGTTCTTT CACGGAATTT ATTCATTCAC CCCAAGCACA 180

ATAAGACATT GCTGTTACAA AAGTCCCAGA CATGCCTGGA GACAATTTTG CGCATCATCC 240

ATTGCATATT TCTGAGTCCA GCTACGAGCA GTGGTTTCC 279

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..172
(D) OTHER INFORMATION: /standard_name= "DB# 164"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCATGGACAA TATCGCCGAC TGGCGGTCAT TCACAGGGAA CTTTTACAGG ACCCAAGAGT 60

TAATTGGTCA GGCTCCAGTC TTCGAACTGA GGCTACTGGC TACGGATTGG TTTTCTTTGC 120

TCAACTTATG CTTGCAGACA TGAACAAAGA ACTAAAAGGA TTAAGGTGTG CA 172

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..155
(D) OTHER INFORMATION: /standard_name= "DB# 165"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAGGAAAGTT TATGCCCCTA TGGGAGCTTT TCGACTGCAG AAACTCACTC AAATTAGTAA 60

TTGAAAATGC ATAGCAAGAC AATATCTCAC AGGCCACATA TAGGCCATAA TAACATGTAG 120

TATGTCTTAT TTAAAGAGGC GAACATTAGA ACACT 155

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..262
(D) OTHER INFORMATION: /standard_name= "DB# 166"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGCAGCTCAA GTGGCATGTG TAATCTCAAT GTTAATAGTC ACTTATAGTA CTGATTGGGA 60

AGGAGCATCC TTGAAGGCAA AACAACTAGT GGGAAGAACT AATGAACTCC CATATGAAGA 120

TCAACTGGTA AAAATTGAGG AGGGTAATGG ATTTCTCAAC GATTTAGCTT CTGAAGTGGA 180

AGGAATCTAA GGATGCAATG GATGCAAGGA AAAGGAAGAG ATGGCCACAG CAGAGAACAA 240

GACATTACAT TCTCTCAGTA TT 262

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..193
(D) OTHER INFORMATION: /standard_name= "DB# 168"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTGTTGATG GTCCAGACGT GCCTGTTGGT GCTGGTGTTG ATGGTCCTAG GCTGACAGTT 60

GGGTTACCAG TAGGTTCAAT TGTAGATTCG GGTGTGCCTG TAGGTGCGGT CGTAGCTTCA 120

GGAGTTCCTG TTGGTGCTGG TGTTGATGGC CCAGGAGTGC CTGTAGGTGC GGTTGTAGCT 180

TCAGGAGGTT CCT 193

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..206
(D) OTHER INFORMATION: /standard_name= "DB# 169"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAACGCTTAT AAAGGTGTTG GCATTGTTTT AGTTACTATT TCCAGTTATT GTCCCTTTCC 60

AGCAGAATAT GTTGTCTTCT TCAGGAAATG CAGATATTCC TGAGTCACCA CTCATCATTA 120

GAGCCATCAA CTCAGATTGC AACCTTTTAA GAACAGACTG AGTATCAACC GTCTTCACAG 180

TAGTCTGTGT CTGCTTTGGT GAAGGT 206

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..318
(D) OTHER INFORMATION: /standard_name= "DB# 172"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGGGGGCAA CACAATATCT AGAATGAACA AAACTTTAGA TATTCGACAG GATAAGAAAA 60

TGGTAAAGGA ACATAATAGT TCTACGAATT CTCAAGTATC TTCTAATCAA TCTAGGGGGA 120

AGGGGACACA TTAACTCTTC CATCTTCACA GGTCTTGGAC GCTCAAACCT GGAGGAAGTG 180

ACTGCTTCAA CTTGTCAGCC TTCTCAAAGT CAGACACACA GAGTGTGTAA AGGATCTGGA 240

GACGCGAACC TTGAACTTAA CCATATCCTT GTTCTTCTTG ATCTTGACAG ATCGTGCATC 300

TTCCTCCTTG CTGTAAGA 318

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..239
(D) OTHER INFORMATION: /standard_name= "DB# 173"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCTTCTTGCT ACTATTGCCT TTTGCAGTAG TATGCAAGAG GCAATAGTAG CAAGAAGCAG 60

AGCTGAAGCC CCAACTGATG ATCCTATAAT GATTTTCTTA CGGCTGCGAT TGGTTTCCCC 120

TTCGTGAAGA TTAAAGTTTC CAGTATAATT CAAAATCACA CCGTTATCAC GAAGACCAGA 180

TGTCCCAACT TACAGATAAT ACATCTTGAG AACAATCAGT TGAGACATCG CTAAATCGG 239

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..224
(D) OTHER INFORMATION: /standard_name= "DB# 175"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACATCCCCCG GAATTCATTC TTCCATAATA GGAAGAGTAT CTTGTAAAGG AAATCTCAAA 60

TTGTAAAATT GACTGCCTTG CCGGACGTAC TAAGTTTAGC TATAACATCT TTTAGAAACC 120

TGCCCATCCA GCAGGTTGGG ACGCTGATTT GCTATCAATA TTCTTTGGTT CACCAAATGC 180

TGAGAATTTT TCGACTCATT GAGAGTGGCC TTTATCTGAG AGCT 224

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..186
(C) OTHER INFORMATION: /standard_name= "DB# 176"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCCGGCTCG GAATATTAAG TTTTAACTAG AAAATTAAAG TCCAAGTGAT TTCAACATCT 60

GATTTCAAAA TTTGAAACAA CCACCGAGTC TAAGATGGCA CGAATCTAAG AGAAGCTTGA 120

ACTAGTAGGT GCACCGCCGC CAAAACCTCC AGTCCAGGCC GAATCCAGGT CTTCCACAGA 180

ACCCCT 186

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..253
(D) OTHER INFORMATION: /standard_name= "DB# 177"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGCGGTGGGT TTGGTGACGA CCAATGGTGG CAGCGAGCTG ATGGACCTCG AAAAAAAGTG 60

ACGGTTTTTG GACGGTGTTT GGTCGGAAAA GGAAAAGGGT CGTTCGGGGT TTCTTTTGGA 120

GTGAATCTGG TGGTTGTTAG GTCCTGCTAA GGTCACGAGC TCATCGGCTG AACTCTGCTT 180

TTCTGCTTCA CCGGAGAAGA TGAAACAATG AGAAAACATT GAATTAGAAC TATGGAGAAG 240

AAAGTCTGGG TGA 253

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..318
(D) OTHER INFORMATION: /standard_name= "DB# 178"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGCCTCTA GATCTGGTGC ACCTGTTAAA AACATAGGTG AGAATCTGCT TATAGCTCGA 60

GCATGGCATT GCTTAAATGT GGATGATGAG GCTAATCGTG GTAGCAGCTG CTGTGAATAG 120

AAGGGCTTTT GATGCCTCTA GATCTGGTGC CACCTGTTAA AACATAGGTG AGAATCTGCT 180

TATAGTCGAG CATGGCATTG CTTAAATGTG GATGATATTT TGGACAAGTC ACAGAAGGAC 240

CAGGCTCAAC CTACATTTGC TCCTGGTGCT CCTCACCAGC CATGATATCC GTCAAGTGTG 300

ATAACCTGGA ATCACCTA 318

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..298
(D) OTHER INFORMATION: /standard_name= "DB# 179"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGACTACAAA CTTTTGATGC TCTATTTCCC TTGTAAGATA CTTATAAGAA CTACAATGTC 60

TTAACAAGGA CAGTTTTGTT CAAACTAAAT ATCCTTGATC CATCTGTCAT GAAAGGATCT 120

GAAAATACCA TTGATTCAGC AAAAACTACA CAAAGGACAT ATACTAGCAA TAAAAGTTGC 180

AGGAACACAT ACTGCCGTCA AAAGAGAGTT CAGGCCAGCG ACAATTGTTC TATTAATCCT 240

ACTGGTATCC CTAGAAGTTA ACTGTAGACA ATCCAGAGTC TGACCACATG TTCTCAGA 298

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..233
(D) OTHER INFORMATION: /standard_name= "DB# 181"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAAGTGGCGT TGGAGGATGA GATAGAGGTG GGACAAGTTG ATTGTGGTAC AGATAAGCCA 60

GTTTGTAATA AAGCATTACA ACAGCTTTTT GTACATGATA ATCAAACATT AATGAACTTC 120

ATTGTCAATC ATAGCAAAGT AACCAATACT GAAATAAGAC AGCTATAGCC AATAGGCCAA 180

GGTGTTCCTC AGTTTCCACT CTTGAATGGA ATGGCTCTTA TGATAACTTG GTG 233

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..258
(D) OTHER INFORMATION: /standard_name= "DB# 182"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CATTGGATTG TTACAGGCTA GAGAACTTGT TAGTGCCCTA CCTGGGATGT TCCCTGGTAG 60

CTTGATGCCT GTACTTCTTC AAGCTGCTGT ACATGTGAGA GAGAACAAGG CTGCTAAAGC 120

TGAAGAAATA TTGGACAGTA TGTAGATAAG TTTCCTGACA GGTCCAAGGT TATCCTGCTT 180

GCAAGGGCTC AGGTTGCTGC AGCTGCTGGC CATCCGAGAT TGCAGCTGAT TCCTTGGCGA 240

AAATACCTAG ATTCAACA 258

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..302
(D) OTHER INFORMATION: /standard_name= "DB# 183"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGGGGTGGGG AGGAAGCAGA CTTCCGGAAG GAGGGGGAAA GAACTCTTAC ACTATCTTGG 60

TTTTCCCTGT ACCAATCCTC TCTTTTTCGC CCATCAAAGT TTGGCGTATA TTCAGTCTTA 120

ACATCCTCAA TTTGTCTACT TCTTGGTAGT TTGTCAGTTC CGGTGTTTTA TTGTATTCCA 180

AAGTTCTAAG TTACCTTGGC TTAAGTGCAA ACTTTAGTTT CTGTAGTAGT TACTATTTGT 240

TTGTGATTTG CTAGACATTC TTTCTCGAGG CATATTTGTT GGTGATAAGC AGGTGTGCCA 300

CA 302

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..288
(D) OTHER INFORMATION: /standard_name= "DB# 187"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ACCAGAAATG CAGATTGATA GAGATGATTC CACAAAGGGA ATCTTAATTG AAACAAGAAG 60

ATATCCTGTG AATATATTTA CAGATTGAGA TAAGACTTCT ATAAAACCTC AAAATTCCTC 120

AATCATCTGA CACCTAGCTT ACTATTTTAC CTGGCTTCTG TCAGCCTATT TATACCAACA 180

AGACCTACAT CTTAAGAAAT TAGAGACAGA TCCTAATAAT TCATCTCACT ACATGTTATT 240

GACATTGCGC CATCTCGTGA TTTTATCCAA AGCAGCAACC TTAGCTCG 288

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..245
(D) OTHER INFORMATION: /standard_name= "DB# 197"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGATGGAATC ACAAAAACAT AATTTACTGA AACCATCCCA AAAATTGGCA TAGGTATAAT 60

AAATATATTG AGGTTAAAAT TGTCAAAATT TGAAGCGCTA ACGACTAACA AATGAAGATT 120

CAGTATCGTA GTAGAGGGTT GCTGTGAGGC GAGGGAGGAG ATCCTTGTGT GAGTGAGATT 180

TGCTTGAATC GATGGACAAT AAAAACTCAT ACAGCTCTTA TAGATCATTC ATGTCACCTA 240

CCTAA 245

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..153
(D) OTHER INFORMATION: /standard_name= "DB# 198"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAGGAAAGTT TATGCCCCTA TGGAGCTTTT CGACTGCAGA AACTCACTCA AATTAGTAAT 60

TGAAAATGCA TAGCAAGACA ATATCTCACA GGCCACATAT AGGCCATAAT ACATGTAGTA 120

TGTCTTATTT AAAGAGACGA ACATTAGAAC ACT 153

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..239
(D) OTHER INFORMATION: /standard_name= "DB# 199"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGTGTTGGAG AATCAATCTG TAGAATACCG CTTACGGATT TCCATTAGAT TTGACCCAGT 60

TAATGGTAGA GGAACGAGGC TTGGTTGTTG ATGTTGATGG TTTTAATGTT GCTATGGATG 120

CTGCCAGGGA AAGATCAAGA AATGCTCAGA GCAAGAATGC CAGTGGTGCT ATTGCCATGG 180

ATGCTGACGC ATCTGCAGCA TTGCACAAGA AGTATCATTT GTTGCAGCGA CCCTTCTTG 239

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..278
(D) OTHER INFORMATION: /standard_name= "DB# 201"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGTCAATCGT TAATTGGATT CAATATGAGT GGCTGGGTTG CTTACATCCA ATCTTTGACT 60

GACAGCTGCA ATGTTATCTC CAGAGCGGCT ATTGTTGGAC TTAATGATGG AGGTAGTGTT 120

TGGGCTCGAA CGGAAGGCGA CAAAGAATTA AGGCTACCGT GTCGGAACTC AAGAAGTTTG 180

TTGAACTCTT TGACAATCTT GATAGTGTTC CAGGAACTGC CGCAGATCTA GAAGGTGTTC 240

ACTACATTGT ACCGAGAACT GAGGAGAACC TCATTTTT 278

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..261
(D) OTHER INFORMATION: /standard_name= "DB# 203"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAAGCCAGAA ATCGATGTTT GATACATGTC TGGCATTGTC ACAGGTGAAT GGGAACTAAT 60

ATGACTTTAC ATCAACAAGA AAAATGTAAA CGCAGCAGGA GCAGTTACAG CTTTGCTAGA 120

AGAAGAAGCA TTTTCTCTAA TAGAAACAGT AAATATTAGC AAATAGAAGG CAAAGGTGCA 180

GAATGTTTAC AGCATTACAG TTGAGCTAAA TTCGAAATAC AGGTTTGATT CTTCTATGCC 240

CCGTCTGACT GACAAAGTTG G 261

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..178
(D) OTHER INFORMATION: /standard_name= "DB# 205"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAACGTTTTA AAAAGTTTTG GAATTAAGTT TTCAACAGCA ATTTCACTAC ATTAATCTGG 60

TCAAAGTAAT ACATTAATAA CTTATTAAAA CTCTCCTAAA ATTCTCATAC TGAACAACTA 120

CATATTCCTC ATAAGTCATA TATTTCATTC CTCTTCCAGT TAGTTTTCTT CTTCACGA 178

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..244
(D) OTHER INFORMATION: /standard_name= "DB# 207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AATCTAAGCT CCAAGAACTA GTCCATAGTT TTTTTTTCTG TGTGCCCTAA AGACCATAAC 60

TTAGAGCCCA AATCTTTTTC TACATCAGCA AAACAACGAT TTGGTGTACC AAACTGTTTG 120

GAACTCGGAC CATTGATGCT AATCATTCCA AGCTGGTGTA GAATTTACGC ATTGGCTGCT 180

GGTTGTAATG GCTCTTCTCT TTCTTCTTGC TGCAGCAAGC CTGGCACTCC CTGCAGCAGC 240

CTCT 244

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..278
(D) OTHER INFORMATION: /standard_name= "DB# 208"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATTTCAAGGT AGGTAATCCA ATACAAAGCT AATATTTGAA GGAACTGTGT TTGCAGTTAA 60

AGACAACTAC AAATAAATGT TCATGTTCAT GGATGGGTTC GGGTAGAGTA TTTTTCAGAA 120

ATAGCAGAGG CGAGAGTGTT GCTATTGTTA AGCCACAGAT GAAGAACCAT TTGCGCCAAA 180

CAATCCTAAA GGATTTGTGG GCAAGCTCTT GGGCAGCCAG GCTTAAACGA TCAGTCAGAG 240

TTGGGAAACA GGGTAAGCGG CCGCATGACA TGCTTGAG 278

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..155
(D) OTHER INFORMATION: /standard_name= "DB# 209"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AAGGAAAGTT TATGCCCCTA TGGGAGCTTT TCGACTGCAG AAACTCACTC AAATTAGTAA 60

TTGAAAATGC ATAGCAAGAC AATATCTCAC AGGCCACATA TAGGCCATAA TAACATGTAG 120

TATGTCTTAT TTAAAGAGAC GAACATTAGA ACACT 155

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..312
(D) OTHER INFORMATION: /standard_name= "DB# 210"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AGCAGAGCCG AATTAAGAAT TAGAAGATGA AAGCATATGC AATTGCACTC ATTGTCTGTG 60

GATCTGTTGC AGCAGCTCTA GTTTTAATAT CGTGTTGTTT TTACAAAATT GGCCGAAAGA 120

AAAAGAGTTC CCCAGTGACT CGGTATGTGA CCAGTGGTTC TCCGGTTATT CCTCTGCCGC 180

CGAAGCCTTT ACCAGCAAAT CGTGATGTTG AAAGGGCGAA ATTAAACCAA GACAATACAG 240

CAATGAGAGA TGGTGGAATG GTAATTCTAG GTGCGGCTGC TGCTGCAACA GTTGTCACGC 300

GTGTTATCGA CA 312

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..186
(D) OTHER INFORMATION: /standard_name= "DB# 212"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCCCGGCTCG GAATATTAAG TTTTAACTAG AAAATTAAAG TCCAAGTGAT TTCAACATCT 60

GATTTCAAAA TTTGAAACAA CCACCAAGTC TAAGATGGCA CGAATCTAAG AGAAGCTTGA 120

ACTAGTAGGT GCACCGCCGC CAAAACCTCC AGATCCAGGC CGAATCCAGG TCTTCCACAG 180

AACCCT 186

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large

Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..189
(D) OTHER INFORMATION: /standard_name= "DB# 214"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCAGTCACAG GAATATATAC TTGAGACTGG GTCTGCAAGG AAATGTTATT GCCCGAACTG 60

ATAGGACGGA TGCTTGTTAT GGGCAATGAA CTTCCTGAAC CATTGACACC ATTTGAACAG 120

TCTTCTTCGG TGGACTCACC GGACTTAGAT GTCGGAGAAT GTGACGCTTC AGATCCCATG 180

TAAAACCTA 189

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..290
(D) OTHER INFORMATION: /standard_name= "DB# 215"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGGAGAACA GTTTAATGAA TATTTTCATT TAGCTCTCAC GTTCATTCTC ATTTACCGAA 60

GCAAAGAGAA TTTTATCAAA ATGGTTCACT GTACATGTAA AGAAACACGC CTATACAAGT 120

GTAAAATTGT TGCTGAACAT GTGAAAACAT ATGTACAAAA CCTATCCTGC ATTCCATGTG 180

GTGCTGTCCG CACCATGGGC ACAACAGAAA CAGTCTACAC GGAGTGCGGC ATAGAGAGGG 240

AGAGCGCATA TGGTCGCGTG AGAGGACCAG CCACACGACT GAGCAGCCTG 290

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..238
(D) OTHER INFORMATION: /standard_name= "DB# 216"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AGAGTAAAGG CAAAGGGTTG TTATTCTGTA AGGTATTCAC TAAATCTCAG TTACTGCAGT 60

ATAAATAGAT GATGGAGGAA ACACTGCTAG CTACATAATT GATCCCCTCC CTATTCTCAT 120

TTCTTGTTCA ATGTATTACC AATGTCTAGC ACAAAACGAT ATTTCACGTC CGATTTCAAA 180

AGACGTTCCA ACGCGGTGTT AACGTACTCA TTGGCACCAT TCAATATCTG GTGTTATG 238

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..260
(D) OTHER INFORMATION: /standard_name= "DB# 217"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAGGCTAC AAAATACATC AAACTTTATA GTAAAACATT CTTAGAAGTC CAAAAATCAC 60

TAGTAAATTC CTGGGATAAC TCTGTAAGGA ACCTTTTCAC AATACAATTT CCAGTACTTG 120

CCATACTTTG CCTTGCATCG GTCATCGTCC CTTTTAGCTC GATCGAGAAG GAGGATTATT 180

AGAAAGATGA CGTAGAAGTA GGGAATGAGT GGTTGAAAAG AGCTGGTACA CTCAGAAAAT 240

GCCGTAATAT TTCTGGACTA 260

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..124
(D) OTHER INFORMATION: /standard_name= "DB# 218"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AAGACCCCAA CAGAGAATTT AGTTGTTATT TGAGGTTGAA ACGAAAGCTA AACGCATTCT 60

TAGCAACTAC CACTTCCTCC CCCTAAAATA AAATAAAACC CAGCATTTTC GAGGTGGTCC 120

TAAC 124

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..263
(D) OTHER INFORMATION: /standard_name= "DB# 220"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAGATGGTGT TTGCTAAGGG AGACCCCGGC ATTGCTGCTT TATACGACAA GCTTCTGGTT 60

TCTGAAGATT TGTGGTCCTT CGGTGAGCTT TTGAGGTCTG ACTATGAGGA GACAAAGAGC 120

CTCCTGCTTA AGGTTGCTGG ACACAAGGAA CTTCTGGAGA ACGATCCCTC CTTAAAACAA 180

CGATTCAGGC TGCGTGATTC CTATATCACT ACTTTAATGT CTGCCAAGCT TACACATAAA 240

GAGGATTCGT GATCCAACTA CAA 263

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..253
(D) OTHER INFORMATION: /standard_name= "DB# 221"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACCGTGAGGG GGATTTTTAG GGGCCTAATT TTGTTGGGAC TCTGTTCCTT GCTACTGGTC 60

GCGCCTTGGT AATATGTAAA AATGGCAGAC GAAGTTTAGG TTGAACAATG AGGAAGCAAC 120

TTTAAACATT TGTAGTCCCA TTAAGCAGAG TGGTGAGCTG CAAATGGTAT CTGCTATATC 180

CTATGGGGTT TAGAGTAGAC CAAGGTACAA ATATAGAGCG CCTTGATATT GAGGCACTAA 240

TGTGTATTGA AGT 253

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..196
(D) OTHER INFORMATION: /standard_name= "DB# 222"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGGGGGCCTC TTTTGTAAAC TTATCTGTGA GCAGTGACCA ACGTCTCTAT AAACCTCAAT 60

CCATCAAATC TGGGCGCAAA TTTATCTGTA GATGTTGATG CTTTCACCGA TTTTGAACAA 120

TCTTCACCAG TTTTCTTCAA ATTATCGTCC TTGTGAAGAG AAATTCGAAC TTTGGATACA 180

GAAGAGACGG TGACCG 196

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..148
(D) OTHER INFORMATION: /standard_name= "DB# 223"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATCCCACTTA GGCTGATAAA GAAATATTAG GGGTAGAGAA TATTCCAGTA TTAATTAAAT 60

TGACTCTACC AATAAGCTTA AGAAAGTCGC TAATTATGAC TGCTCAAAGT TCCTAAGACA 120

AGTCCAGGTG AAGGATTTCT TATGCAAG 148

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..99
(D) OTHER INFORMATION: /standard_name= "DB# 224"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAGTTATGAA CTTACTTTAT GATATTCAAA TACGAACAAG CTAAAAATAT GTTTAGCTTT 60

ATTTTCAGGA CATAAGAGTC ATACATCGTT CAGCGCTTG 99

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..226
(D) OTHER INFORMATION: /standard_name= "DB# 226"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AAGAAAGAAA AAAAGAGGTG AAGAAATTGT AAGAAAAACT GTTGTTACAA GGAAATGTCA 60

CTTCACCATT AAAATTTTGG AAAAAACATG GACACAATCC CTTTCAATGG GTGGTGCTTC 120

AAGATATAAC ATAACGAAGT TAAAGAAATA GATGAGAGGG GGGAAAGACA ACACAAGACA 180

ATGTTTTCCC CCTTTATATT AAAAGACATG TTTTTTTGTT TTATGT 226

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..276
(D) OTHER INFORMATION: /standard_name= "DB# 227"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CACATGCTGG CAAGGGTATA TTAGCACGTC CATCACTGAT GGTCCTGGAT GCTTGATGTT 60

GCGCTGTCCT GCTCCAGGGT GTGATTATGC AGTTGACTAT ATTGTTGGTA GTGGAAGCTA 120

TGATGTTACT TGTGGGTGCT CATATAGTTT CTGCTGGAAT TGTACCGAGG AACTCATCGC 180

CCAGTTGATT GTGGAACTGT GTCTAGTGGA TTTGAAGAAC AGTGCAGAGT CTGAGAACAT 240

GAACTGATAT TAGCTAATTC TAAGCCTTGT CCGAAT 276

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..245
(D) OTHER INFORMATION: /standard_name= "DB# 228"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGTGCAGTTA CTCTATCTTT GCTATAGCCT GGTTGTCATA AAGTTGTGGT GCATACAAAA 60

GTTTGGATAG TTTCCAAAGA TGTGAAGATG ATTAACTATT TTATCACTTT GTAGGAGTGG 120

AAAAGGGCTC GAAGGACCCA CAGAGGGAGA AAGTGGGGAA AATAACTATT GATCAATTGA 180

AGGTAATTGC TCAAGAGAAG TTGCCGGATC TTAATTGTTC TACTATTGAA TCTGCAATGA 240

GGATA 245

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..233
(D) OTHER INFORMATION: /standard_name= "DB# 230"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAGCCAAGTT TCTATGACCA GAAGCAGTCA CATACAAGTC CATGCTCAGT AATTATAGAA 60

GCAGTCACAT ACAAGTCCAT GCTCAGTAAT TATAACTGTT TCGCCACATC AAAATTCAAT 120

ATCTATCATA TAGAGCTGTG CCAAAGGCAA ATAAACATAA CTGTTTTTGC CCAAGCTAAA 180

TCTAACGTAA CGACTTTCAA TTGCCTCGTA TTGGGATCTG CCATCACATA ATG 233

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..174
(D) OTHER INFORMATION: /standard_name= "DB# 231"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CGGGACCACA GAAACACAAC ACACACCGGA TACAGAGAAA CAAGGACCGG CATTGTCTTC 60

TGTAGGACAG ACACAACGAC TTCAACCAAG TTCCACAGAA ACTAGGACCC GGACTCAAAC 120

AAAACCTTCA CCGTAAAGTT CCACACGTTA AACAACAATA TCCACCCTAA GAGT 174

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..287
(D) OTHER INFORMATION: /standard_name= "DB# 232"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AAGAGAACGA AACGCACGTA ATGGTTATCA TAGCTTTCCA CAATTTCACA TTAACCAAAA 60

CAATTGCACT ACTTGTAGGC TAATGAACTG GTGATGGTTG AGAAACTGGA GATGTTTATT 120

AGTGAAGGAA AAACACAGAA CAGGTTTAAA CACACTGGAA ACATAAATAA 'CAGAAGACTG 180

CTGCAGAAGT CACACTGAAC TCATACCAAA GACCATTTCA ACTGCTACAT TAGACTAGAA 240

GAGACCTTCC ATGACTGCCA CAGCTTCCTC TCAGCATACC TCTGCTC 287

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..277
(D) OTHER INFORMATION: /standard_name= "DB# 233"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACCCATCAAA AAGTGTATTT ATACTCTCAG TGCACATATG TTCAGCACTC GTGCTGTCTG 60

ATCTAGGGCC AAAACTGCGC ACAGGTCACA ACCTGCAATC ACCTCATTAC ACATTTGAGA 120

AATGAGCAAA ATAATACTTC CACATTCAGC ATAAAACAAA AGTTCATCTG ACGTTGAATC 180

TGTTTAAGAA TGAGATGATG AATCTGTTTT CTCAGCCAAA TAGTGCTCAA GCATATCTCT 240

CATCATCATC TCACTCATCA CTCGAATCAT ATCATCC 277

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..255
(D) OTHER INFORMATION: /standard_name= "DB# 234"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGGCCCTCA ACTAAGTTGG CCAATTTATT GGATCATTTT AATTAACTAA TAACTGAAAT 60

ATCAGAGAGA CAACGTTCCT CATATCTGCA AGAAGCTAAA AAGGCGGCAA CGTCGGTGCC 120

CTTACATGTA TGTGCTGCAC GACCTTAAAA AGTCAAAATT TGAAAGAAGA TGATCTTCCT 180

ACATATTTAC ACTGTTTGTA GCAAAAGAAC ACCGCAAAAG AAAAATCCTG TCTCATCATC 240

GACAAGCAGG TGCCA 255

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..202
(D) OTHER INFORMATION: /standard_name= "DB# 236"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAGAAGGGGG AAAGGGGGAG CTCGGAGGGA GGGTGAGGAA ATGTTTACAC CCTCTCCCCC 60

GCATGCTGAG GTCCCTCCAC CAACTTAAGG AAGCAAAATT ACTACAGCAA ATTTCTGAAA 120

TTTAGCAAAG AGGAACAAAA CAATTGCAAC CACTGATTTC CTGCTTGTCT GCTTGGCCGG 180

GTGTGCGTCG CCGTGTTGGG CT 202

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..77
(D) OTHER INFORMATION: /standard_name= "DB# 239"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGTGAAGGCG GCGGCGGCGG CAGAGGAGGT ATGATTATTT TGGTGTTTAG AGGGCATGGA 60

GGGTCACGTG TAGCGAA 77

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..222
(D) OTHER INFORMATION: /standard_name= "DB# 240"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AAAGCAACAC AAACCTCTTC ATTTCATCTG GCAAAAAAGT ACAATCAATC ACTCAAAATT 60

GACTTATAAC TCATAACAGT AGGAATCCTA AATAGATGGG AAATTAACAG AAGCATTATT 120

CAATGAACTG ACAAAGACAA TATGTCATCA TGTAAGGTCT AATGAACCAA AAATGCAATG 180

CTGATATGGA AATGAAATTA GTAGATTGAG ATCTTCTCGC AG 222

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..309
(D) OTHER INFORMATION: /standard_name= "DB# 241"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CCAAGATACT GATTACTGTT TTCTGTTGAA CCGGCATGTC TGTATCTTGT GTATATAGTT 60

TAATTCTGGA GCATGATGGC TAAAATGAGA TCTTGATAAC TAGGCATAGT AATTGATAAA 120

TGTGTGTCTT TAAGCATGAT ATAGAGGTAC ACCACAGCAT TACCCTAAGT CTAAAATTCA 180

AACTAGGTGT CTAATAATCT GGTAGAGTGA TGAGAGTTCA AGTGAGTGTG AGGAAGATTT 240

GAATAGTCCA TATTTGTACT GAGCTAGAAC TTGGCTGATC CTGAGCCTGT ATTACGCTAA 300

GAAGTCCTA 309

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..246
(D) OTHER INFORMATION: /standard_name= "DB# 244"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGAAGTGCTG GAGGCCCTTC TTCTGCAACA ATAGTCTTCA CACAATCAAC AATGCTCTTG 60

TATTGATTGG CAGAACCCTG AGTCATTAAT CTCGTCTTAA TGACATCAAG AGGAGTAGTT 120

ATAGCTCCAG TTAGAGCACC AGCAAAAGCA CCGATAACTG CATTCTCTGG ATCATTCAAT 180

TCCCTTTTTG CAGCCAGCTT ATAACCTATC CGCAGCTGCT CATAGTAACG ACTGGATGGC 240

ATCAAC 246

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..205
(D) OTHER INFORMATION: /standard_name= "DB# 246"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGAGGAGA ACATCTCCGT GTTGCTGAAG TTTGCCTTCC AGGTCGTCTA TTTTCGACGT 60

TGGTGGTTGG ATCACGCGTC CGTCGGAGCT CGGAGGTTTC ACCTGAGACG ACGTCGCCGC 120

AGCTGGCTTT GCGGTTGTTT CTCCACGAGT TCACTGGGAC TGTTTGGTTG CTCACCGAGA 180

GCTCGTGCTT TGTTGTTGTT GTTGC 205

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..107
(D) OTHER INFORMATION: /standard_name= "DB# 247"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGCGGCGTTG TGAAGCCTTA TCATGCTTAT ACGCCATCTG GGTAGCGTAT GGTGAGCCTT 60

TTTTTTGAAG TTATGGGAAG GAAAAGGACT ATATTCCCCT TGGTCGA 107

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..209
(D) OTHER INFORMATION: /standard_name= "DB# 249"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

AGACCCACAA ATCAAACTCA AACAAATTCA ATTTAGAACT CATTGGATAA AGGAGCATGT 60

TCTTGTGTCA TGAACACATT TGTGTAAATA AGACCAGCCA AACTACCACC AACTAATGGA 120

CCAATCCAGT AGATCCAGAA ACCCTCAAAG TTACCACTAA CCATTGCAGG TCCAAATGAA 180

CGAGCTGGGT TCATTGATCC ACCGGAGAA 209

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..199
(D) OTHER INFORMATION: /standard_name= "DB# 250"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTCACATATC AATGATTTTC TAGCGGACGG CAAAATCCTT ACAAGTCTAG AAACTCAATG 60

ATGTGTAAAG GCTCAATCCA TGCGAGCAGA ATAAAACCCT AGATACCATA GAGGGAGAGG 120

AGGAAAACGG AGAAAGCAGT GGTGGGACGA AGCTTACTGG ATTGGAATGT GTGTAGGTGG 180

AGTGATGGAT GGACCTGAA 199

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..211
(D) OTHER INFORMATION: /standard_name= "DB# 252"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTAATAAA TCTCCATTCA TTTCCATTCA AGAGAACTTT GTAAACAAGG ATCCACAGGG 60

TAACATCACG GTAACAATAG AGGTCAAAAG CAGAACACTA ACAGTAACCA GGGCAAAACC 120

ATAAACGTAA CTTCATCAAC ACTTCGAAAC CATAAGTAAG TTCAGACGAG ACCAATCTAA 180

AAAGCCAACA GAAAATCTAA TCCTTATCGG C 211

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..203
(D) OTHER INFORMATION: /standard_name= "DB# 255"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TGAATATGAT GGCCCTCGTA AGATTTAATA TGAATTGAGC CTTTGGAGTT TGAATATGAA 60

TGATGATCTT GGCGATTTGA ATATGAATGG CCCTTTGGCG TCTTGAATGG CAATGGCCTT 120

TTGGCATTTG AATATGATGA CCTTGGCAGC TTGATATATG CTTTGGCATT TATATGATGC 180

TTTGGCAGTT TGAGTAGCGG CCG 203

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..184
(D) OTHER INFORMATION: /standard_name= "DB# 256"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCCTATCACT CAGATTGCTA AAAAAAAAAC ACTTCCATTT GCAGCATCTG ATTACCACAA 60

TTTTTCCTGG TAATTCAAAA AAAAAAAACC ATACTATTAC ATTAAAGGAC GAACCTTTTA 120

GTTGAAATAA TTGTCACCAC GAATATGAAA CTGGACTTCT AACTTGGTTT TGAGCATTGT 180

TACC 184

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..188
(D) OTHER INFORMATION: /standard_name= "DB# 263"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGGGTCGCAT GTTGGTAAGG AGCCACAGAA GTTTATTGAT GAGGTCAATA AAATATTTGG 60

TATGATGTCA ATAACTGCGT CGTTATAGGT GAGATTGGCA TCCTCCAAAC TCAAGGATCG 120

TGACGCACAT AGGTTTACTC AGTGGAAAGA CACAACATGA TTTTGGAGAA CTCAGTAAGC 180

GGCCGCAT 188

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..193
(D) OTHER INFORMATION: /standard_name= "DB# 264"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTTGAGGATC TGAATCAACC TCGTCAAATG CTCGTGGAGA TGCTTTGTGA AGAACGCGGT 60

CTATTTCTGG AAATAGCTGA CATAATAATA GGATTGGGCT TGACCATCTT AAAAGGGGTT 120

ATGGAAACGA GGAACGACAA AATATGGGCG AAATTCGCTT AGAGGCAAAT AGAGACTACG 180

AGATGAATAT TCA 193

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..218
(D) OTHER INFORMATION: /standard_name= "DB# 265"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGATGCTGAT CTTGGTGGGG ATGTTGACTC GAGCAAGAGT ACGTCCGGGT ACATTTACAC 60

CATAGGTGGA AAAGCAGTAA GTTGGATGTC CGTGTCTTTA GAAGTATGTT TCTCTTTCAT 120

CCACTAAAGC TGAGTTTGTG GCAATAGCTG AAGCTGGGAA AGAGATGATA TGGATGGCAG 180

ATTATCTTGA GGAATTGGGC AAGAAGCAAA GCAGAATT 218

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..193
(D) OTHER INFORMATION: /standard_name= "DB# 266"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGCAAACAAA GTAGAATTAC ATTGCAGTTT CTCCCTTACT AGTCATCAAA TAAATATTCA 60

CAAATTGAAA CACAGCTGTT CCCTTAACAA CCCTATGAAG GGAGATTAAG AAGTAACTAA 120

GTTCGTTTCA CGGAACCTTT ATTCATTGCA CCCCAAGCAC ATAGACATTG CTGTTACAGT 180

CCAGCTGCTC CGG 193

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..131
(D) OTHER INFORMATION: /standard_name= "DB# 275"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGATCATCA ATGACCGGGA AACTGGTAGA TCTAGAGGAT CTTGATGGTC GCAACATCAC 60

CGTGAACGGA GCTCAATCAC GCGGAGGGGC TGGAGGTGGA GGTGGAAGAG GCGGGGGTGG 120

TTAGGAGGTG C 131

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..220
(D) OTHER INFORMATION: /standard_name= "DB# 277"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCAGTGGGCA CATTGTTAGG AGCAATGACA GGAGCTTTGA TAGGTCAAGA AACTAAAGTG 60

GATTCATTAG AGGTGCCGCG GTTGGAGCCA TTTCTGGTGC TGTTTTCTCT CTTGAGGTCT 120

TTGAGTCATC TCTGATACTA TGGCACTCTG ATGAATCCGG AGTTGGATGT GTTCTGTACT 180

GATTGATGTA ATAGCTAGCT TGTTAAGTGG TAGACTAGTT 220

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..323
(D) OTHER INFORMATION: /standard_name= "DB# 279"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AACTAAGAAT GCTTAGATGC TGAAATAACC TTGCATGTTG AAGCAACACA AAAACTGAAT 60

AAAATTTTGA CAATGTCCTA ATATCACAAG GACACGAATA GGCAAGTGAA CATACCCATA 120

TCTCTAATGC AGAGCCCTAC TGATCCAAAT ATGAACATGG ACTACATGGT TAAAAATTTT 180

ACACTCAGAT GAATTAAGCA AGTTGGCACA GAAGAGGTTT TGGTGCCCAA CAGAAGAGTG 240

GATCTCACCA AGAGCCGCCT CTACCAAGGT TTGAGGTCAC CAACTGGCCA GCAGTCCAGT 300

TTAAGGCTCT CCCCGGCTTC AGT 323

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..336
(D) OTHER INFORMATION: /standard_name= "DB# 280"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATCTAACAGT TGAAGGAGCA GAAGAATTAG AAAGCCACGG AGGAAGAAGA GTTTGTGGCG 60

TAGGAGTTGA GGCATCGGCG TGGAGGAAAC CTCCATTAGA AGTAGCCATA GGTAAACCTG 120

GGACACTCCT TTCTTTCACA ATCTTTTCTG CAAAGGTTTC GAGAACGTGA TCGTATTTTC 180

CATCGTCTAC TGGATCACAC CTTGTTGTTT TCTTTCTGCT CTCTCTGTTG CCTTCTCTTT 240

GAAACTTCCC ACCACTTTCC TAATCTTTTA GCAGTTCGAC CTGGTACTTC AGCTGCTATT 300

TTTCTCCATT TGTTACCGTG TTTGGCTTGT AGTTGA 336

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..278
(D) OTHER INFORMATION: /standard_name= "DB# 288"

(xi) SEQUENCE DESGRIPTION: SEQ ID NO:106:

ACTTGAGAAA TACTTTGTTT AGTCTAAAAC AGGAAAAAGT ACAATTTGCC TTCTGGAGAA 60

GAATAAGATC TTTGTCTCAA CTCACAAGCT AATAATACTA AACAAGCAAA TGAAAGGGTA 120

GAAAACCTAG CTAAAGAGCT TCAGGAAAAC AGATAATACA TGCCAAACGG CAATAATATA 180

GTATTCCAAG TTGCGCATCA CCCATAGCAA CACCATGACT TCCATTACAC ATGACTGGAA 240

ACTTATTGGT AACCAAAATT ATGGGTATCA GCGCAGCC 278

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..175
(D) OTHER INFORMATION: /standard_name= "DB# 289"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TACTCACTAG GAGCACAAGG TTGAAGTTCT ATTTATAACA AAAATATGGA ATAAAACAGG 60

AAAGCAAAAC TTCAAAATTC AAAACACAAG GCACTTCCAT TAAAGTGCTT TCATGAAATT 120

CTAAATTCTC CTCAAAATTC TAAACAGGAA AACTAATTTA GACTGATCCG ATTTT 175

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..112
(D) OTHER INFORMATION: /standard_name= "DB# 291"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTGAATTTCT AGAGCGTTGT GAGCAAGATG ATGGATTTCT TGAAGGTTTT ATGAGGAAGA 60

GTAGATGGAA TGACGGGCAT GCTTCCAAGT CAGCAAAGGA CGATGGGAAA GA 112

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..825
(D) OTHER INFORMATION: /standard_name= "DB# L23762"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTCTTCTTCC ATTTCTTTCA AAATTAAAGT ATTGTTACTC TGCTATTGGC TCAAAACCTC 60

TGCAATCTCC GTCTCCTTCA ATTTCAACTC AAGCAAATCC ACCTCTTTCA CTAGTTTCAT 120

CACTTTCAGA TCAGGGTTTG GAGTTGAAGG TACGGGGGGC TAATTGATGG CGTCGAAGAG 180

GATATTGAAG GAGCTCAAGG ATCTGCAGAA GGATCCCCCC ACATCATGCA GTGCTGGTCC 240

AGTGGCAGAG GATATGTTCC ATTGGCAAGC AACAATCATG GGGCCTACCG ATAGCCCTTA 300

TGCTGGAGGT GTATTTTTGG TTTCAATTCA TTTCCCTCCA GATTATCCTT TTAAGCCTCC 360

AAAGGTTGCC TTCAGAACTA AGGTTTTCCA TCCCAACATC AACAGCAATG GAAGTATTTG 420

TCTGGATATT CTTAAGGAGC AGTGGAGTCC AGCATTAACC ATATCCAAGG TCCTGCTGTC 480

CATCTGCTCT CTGTTGACAG ACCCAAACCC AGATGATCCT CTTGTACCTG AAATTGCTCA 540

CATGTACAAG ACTGACAGGG CCAAATACGA AACCACTGCT CGTAGCTGGA CTCAGAAATA 600

TGCAATGGGA TGATGCGCAA AATGTCTCCA GGCATGTCTG GGACTTTGTA ACAGCAATGT 660

CTTATGTGCT TGGGGTGAAT GAATAAATTC CGTGAAAGAA CTTAGTTACT TCTTAATCTC 720

CCTTCATGAG GGTTGTTAAG GGAACAGCTG TTTTCAATTT GTGAATATTT ATTTGATGAC 780

TAGTAAGGGA GAAACTGCAA TGTAATTCTA CTTTGTTTGC CAGTT 825

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligo)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /standard_name= "P35"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTAAGCGGCC GCAGCGTCAG TAACTC 26

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligo)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /standard_name= "P36"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TACTGACGCT GCGGCCGCTT AC 22

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /standard_name= "P39"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ACTCTTGGGC CGAGTTGGCC TTTTTTTTTT TTTTT 35

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..24
(D) OTHER INFORMATION: /standard_name= "P40"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ACTCTTGGGC CGAGTTGGCC TTTT 24

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..18
(D) OTHER INFORMATION: /standard_name= "P46"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GGCCAAGTTG GCCTTTTT
18

WHAT IS CLAIMED IS:

1. An isolated polynucleotide capable of hybridizing under stringent conditions to a nucleic acid having a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 18, SEQ. ID. No. 20 through SEQ. ID. No. 33. SEQ. ID. No. 35 through SEQ. ID. No. 45, and SEQ. ID. No. 47 through SEQ. ID. No. 109.

2. A composition comprising an isolated expression cassette having a nematode-responsive promoter operably linked to a polynucleotide encoding a polypeptide that inhibits nematode infection, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 109.

3. The composition of claim 2, wherein the polypeptide inhibits signal transduction associated with feeding cell formation.

4. The composition of claim 2, wherein the polypeptide is an antibody.

5. The composition of claim 2, wherein the polypeptide elicits a defense response against plant pathogens.

6. The composition of claim 2, wherein the polypeptide is toxic to plant cells.

7. The composition of claim 2, wherein the polypeptide is toxic to nematodes.

8. The composition of claim 2, wherein the nematode infection is caused by root knot nematodes.

9. A composition comprising an isolated expression cassette having a nematode-responsive promoter operably linked to polynucleotide which inhibits expression of a nematode-induced gene, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID No 1 through SEQ ID No. 109.

10. The composition of claim 9, wherein the polynucleotide is linked to the promoter in an antisense orientation.

11. The composition of claim 10, wherein the polynucleotide is selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 109.

12. The composition of claim 9, wherein the polynucleotide transcribes a ribozyme.

13. A nematode-resistant transgenic plant comprising an expression cassette having an isolated nematode responsive promoter operably linked to a polynucleotide encoding a polypeptide which inhibits nematode infection.

14. The transgenic plant of claim 13, wherein the polypeptide inhibits signal transduction associated with feeding cell formation.

15. The transgenic plant of claim 13, wherein the polypeptide is an antibody.

16. The transgenic plant of claim 13, wherein the polypeptide elicits a defense response against plant pathogens.

17. The transgenic plant of claim 13, wherein the plant is a tomato plant.

18. The transgenic plant of claim 13, wherein the polypeptide is toxic to plants.

19. The transgenic plant of claim 13, wherein the polypeptide is toxic to nematodes.

20. The composition of claim 13, wherein the nematode infection is caused by root knot nematodes.

21. A nematode-resistant transgenic plant comprising an isolated expression cassette having a nematode-responsive promoter operably linked to polynucleotide which inhibits expression of a nematode-induced gene, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID No 1 through SEQ ID No. 109.

22. The composition of claim 21, wherein the polynucleotide is linked to the promoter in an antisense orientation.

23. The composition of claim 22, wherein the polynucleotide transcribes a ribozyme.

24. The transgenic plant of claim 21, wherein the polynucleotide transcribes a ribozyme.

25. The transgenic plant of claim 21, which is a tomato plant.

26. A method of conferring nematode resistance on a plant, the method comprising introducing into the plant an expression cassette having a nematode-responsive promoter operably linked to a polynucleotide encoding a polypeptide that inhibits nematode infection, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 109.

27. The method of claim 26, wherein the expression cassette is introduced into the plant using *Agrobacterium.*

28. The method of claim 26, wherein the plant is a tomato plant.

29. A method of conferring nematode-resistance on a plant, the method comprising introducing into the plant an expression cassette having a nematode-responsive promoter operably linked to polynucleotide which inhibits expression of a nematode-induced gene, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 109.

30. The method of claim 29, wherein the expression cassette is introduced into the plant using Agrobacterium.

31. The method of claim 29, wherein the plant is a tomato plant.

FIG. 1

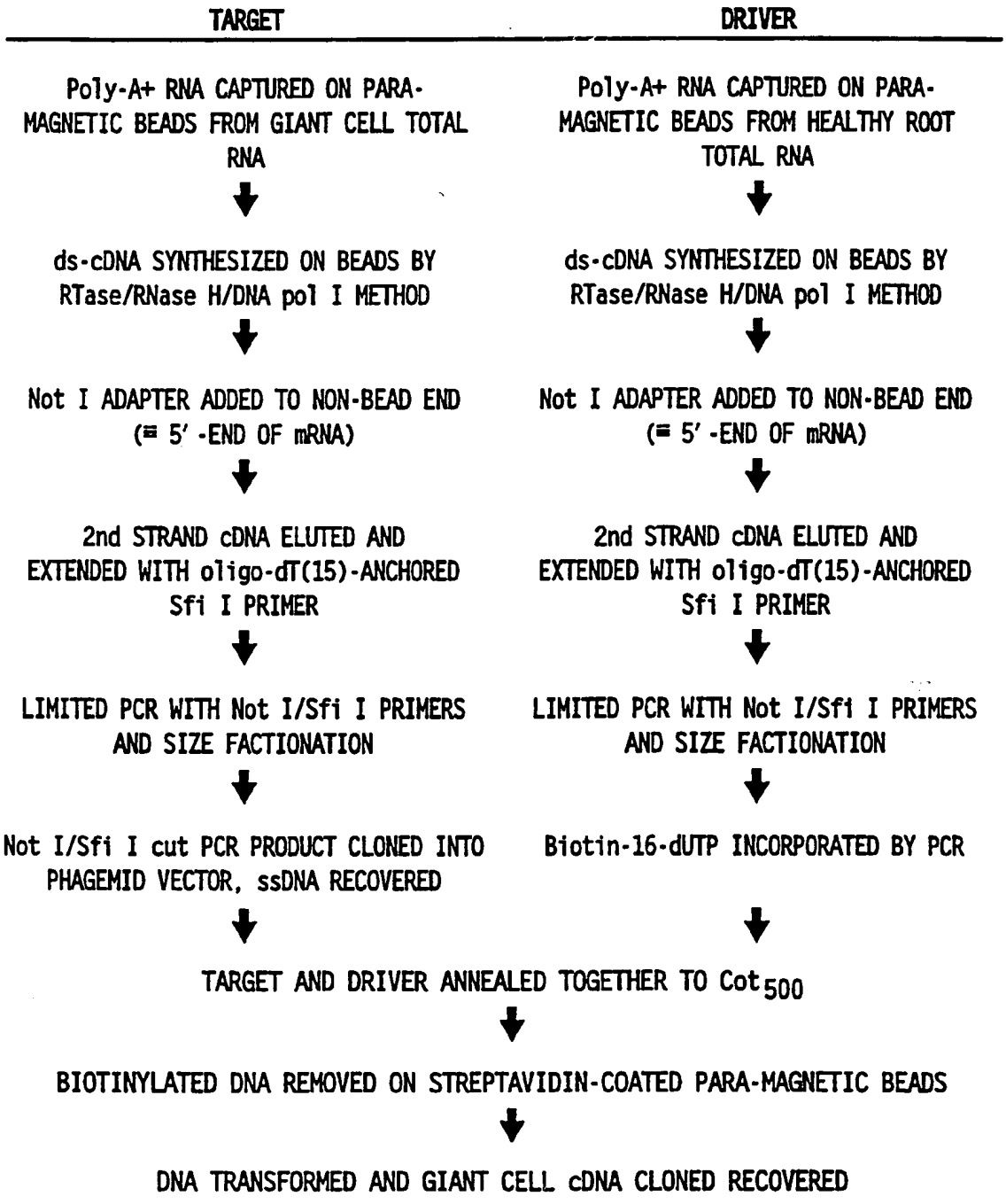
TARGET
DRIVER
Poly-A+ RNA CAPTURED ON PARA-MAGNETIC BEADS FROM GIANT CELL TOTAL RNA
Poly-A+ RNA CAPTURED ON PARA-MAGNETIC BEADS FROM HEALTHY ROOT TOTAL RNA
ds-cDNA SYNTHESIZED ON BEADS BY RTase/RNase H/DNA pol I METHOD
ds-cDNA SYNTHESIZED ON BEADS BY RTase/RNase H/DNA pol I METHOD
Not I ADAPTER ADDED TO NON-BEAD END (≡ 5′-END OF mRNA)
Not I ADAPTER ADDED TO NON-BEAD END (≡ 5′-END OF mRNA)
2nd STRAND cDNA ELUTED AND EXTENDED WITH oligo-dT(15)-ANCHORED Sfi I PRIMER
2nd STRAND cDNA ELUTED AND EXTENDED WITH oligo-dT(15)-ANCHORED Sfi I PRIMER
LIMITED PCR WITH Not I/Sfi I PRIMERS AND SIZE FACTIONATION
LIMITED PCR WITH Not I/Sfi I PRIMERS AND SIZE FACTIONATION
Not I/Sfi I cut PCR PRODUCT CLONED INTO PHAGEMID VECTOR, ssDNA RECOVERED
Biotin-16-dUTP INCORPORATED BY PCR
TARGET AND DRIVER ANNEALED TOGETHER TO Cot500
BIOTINYLATED DNA REMOVED ON STREPTAVIDIN-COATED PARA-MAGNETIC BEADS
DNA TRANSFORMED AND GIANT CELL cDNA CLONED RECOVERED

FIG. 2

K PSSDS
YK PSYDNS
YKKPSYDSG
YK PSYDNG
YKKPSYDSG
YK PSYDS
YK PSYDN
YK PSYDS
YK PSYDN
YK PSYDRL*

TS PSYSP

FIG. 3

DB#280:		QLQAKHGNKWRKIAAEVPGRTAKRLGKWWEVSKRRQQREQ
PETUNIA Ph3	[Z13998]	+L AK GNKW ++AA++PGRT + +W +R+QR
MOSS	[S24244]	L A GN+W +IAA++PGRT + +W +++ R Q
SNAPDRAGON 315	[JQ0961]	+L A GN+W KIA +PGRT + +W +++
BARLEY HV33	[P20027]	GN+W +IA+ +PGRT + +W +++ R+Q
SNAPDRAGON 308	[JQ0960]	+L + GNKW IA +PGRT + +W RR+
ARABIDOPSIS MYB1	[D10936]	A HGNKW IA +PGRT + W + RR+
MAIZE Zm.P1	[P27898]	+L A GN+W IA+ +PGRT + +W RQ
DROSOPHILA	[P04197]	Q + GN+W KIA +PGRT + W + RR+
HUMAN	[M13666]	Q + GN+W +IA +PGRT + W + RR+ ++

FIG. 4

```
TOBACCO: TGACCAGATAAAAACAAATTTGTCTGATAAAGGGGGAAAACTTTTATCTTCTGTGATCTTCCCCCCATC...
         |  | | |||||||  | | |     || ||||| |||   || |||| |||  |||| ||||| ||
DB#226:  ATAAAACAAAAAAACATGTCTTTTAATATAAAGGGGGAAAACATTGTCTTGTGTTGTCTTTCCCCCCTCTCA

TOBACCO: TATTTTTACTTAACTTCGTTATGTATTTTGATTTTGAAGCGCCGCCCATTGAAAGGGAGGGATTGTGTCCAA
         | | |||  ||||||||||||||||   ||  || |||||||  || |||||||||    ||||||||||||||
DB#226:  TCTATTTCTTTAACTTCGTTATG...TTATATCTTGAAGCACCACCCATTGAA....AGGGATTGTGTCCAT

TOBACCO: GTTTTTTCCAACATTTTAATGGTGAAGTGACATCTCCTTGTAACAACACTACTACTCTTCCAAATTCACCTC
         ||||||||||| ||||||||||||||||||||||| |||||||||||||| |  |  |||| ||| |||  | |
DB#226:  GTTTTTTCCAAAATTTTAATGGTGAAGTGACATTTCCTTGTAACAACAGT..TTTTCTTACAATTTCTTCAC

TOBACCO: CTCTTTCTTTTTTCCTTGTTTTTCATTTGATGAGN(24)-ployA
         ||||||  ||| || |||
DB#226:  CTCTTTTTTTCTTTCTT-polyA
```

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/06505

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12N 15/29, 15/82; A01H 4/00
US CL : 536/24.1, 23.2, 23.6; 435/320.1, 172.3; 800/205
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/24.1, 23.2, 23.6; 435/320.1, 172.3; 800/205, DIG 44

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN Biosis, SDC
Search terms: SEQ ID NO: 17, nematode(s), promoter(s), inducible, induced, responsive

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Science, Volume 263, issued 14 January 1994, C.H. Opperman et al., "Root-knot nematode-directed expression of a plant root-specific gene", pages 221-223, see the entire document.	1-31
Y	Journal of Cellular Biochemistry, Supplement 0 (18 Part A), issued 09-16 January 1994, O.J.M. Goddijn et al., "Analysis of gene activity in nematode-induced feeding structures, using promoter-GUS fusions and promoter tagging", page 93, abstract X1-133, see the entire abstract.	1-31

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search	Date of mailing of the international search report
10 JULY 1995	05SEP1995
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer CHE SWYDEN CHERESKIN Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/06505

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Journal of Nematology, Volume 25, Number 4, issued December 1993, C.L. Cramer et al., "Regulation of defense-related gene expression during plant-pathogen interactions", pages 507-518, see especially pages 513, column 2 to page 514.	1-31

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/06505

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-31

Remark n Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/06505

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

SEQ ID NOS: 1-109

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: SEQ ID NOS: 1-109 constitute a group of nucleic acid sequences which share neither the same structure nor function (see description, Table 1). Thus an objection of one sequence would be unlikely to be applicable for any other sequence in the group. Thus, each sequence is drawn to a different inventive concept. Accordingly, the claims are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept. Applicants have elected the species SEQ ID NO: 17.